

GenCode version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 13, 2003, 06:09:06, Search time 57 Seconds
(without alignments)
199,936 Million cell updates/sec

Title: US-09-905-744b-6

Perfect score: 2250
Sequences: 1 MATHSGTFFVFLVVCVCSN.....ETGVALGATHLLOSIGISH 428

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 83025

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: sp:archaea.*

2: sp:bacteria.*

3: sp:fungi.*

4: sp:human.*

5: sp:invertebrate.*

6: sp:mammal.*

7: sp:nhc.*

8: sp:organelle.*

9: sp:plant.*

10: sp:rodent.*

11: sp:virus.*

12: sp:vertebrate.*

13: sp:unclassified.*

14: sp:unclassified.*

15: sp:virus.*

16: sp:bacteriophage.*

17: sp:archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2236	99.4	428	Q9EXX0	homo sapien
2	1900.5	88.5	427	Q9EXX0	homo sapien
3	1900.5	88.5	427	Q9EXX0	homo sapien
4	1984.5	88.2	427	Q9EXX0	homo sapien
5	996	44.3	483	Q9EXX0	homo sapien
6	996	44.3	483	Q9EXX0	homo sapien
7	696.5	31.0	463	Q9EXX0	homo sapien
8	696.5	31.0	463	Q9EXX0	homo sapien
9	616.5	27.4	479	Q9EXX0	homo sapien
10	616.5	27.4	479	Q9EXX0	homo sapien
11	538.5	23.0	558	Q9EXX0	homo sapien
12	538.5	23.0	558	Q9EXX0	homo sapien
13	515.5	22.9	529	Q9EXX0	homo sapien
14	515.5	22.9	529	Q9EXX0	homo sapien
15	515.5	22.9	529	Q9EXX0	homo sapien
16	503.5	22.4	467	Q9EXX0	homo sapien

17	498	22.1	462	10	Q9EXX0	homo sapien
18	494.5	21.8	456	10	Q9EXX0	homo sapien
19	489	21.7	455	10	Q9EXX0	homo sapien
20	489	21.7	455	10	Q9EXX0	homo sapien
21	488	21.7	455	10	Q9EXX0	homo sapien
22	488	21.7	455	10	Q9EXX0	homo sapien
23	486	21.6	455	10	Q9EXX0	homo sapien
24	486	21.6	455	10	Q9EXX0	homo sapien
25	485	21.6	455	10	Q9EXX0	homo sapien
26	484	21.4	455	10	Q9EXX0	homo sapien
27	484	21.4	455	10	Q9EXX0	homo sapien
28	475	21.1	468	10	Q9EXX0	homo sapien
29	473	21.0	467	10	Q9EXX0	homo sapien
30	472	21.0	467	10	Q9EXX0	homo sapien
31	472	21.0	467	10	Q9EXX0	homo sapien
32	465	20.7	447	10	Q9EXX0	homo sapien
33	464.5	20.6	558	3	Q9EXX0	homo sapien
34	462	20.5	466	10	Q9EXX0	homo sapien
35	443	19.7	473	10	Q9EXX0	homo sapien
36	436.5	19.4	556	3	Q9EXX0	homo sapien
37	435.5	19.4	556	3	Q9EXX0	homo sapien
38	435.5	19.4	556	3	Q9EXX0	homo sapien
39	425.5	18.9	555	10	Q9EXX0	homo sapien
40	424.5	18.9	555	10	Q9EXX0	homo sapien
41	424.5	18.9	555	10	Q9EXX0	homo sapien
42	424.5	18.9	555	10	Q9EXX0	homo sapien
43	397	17.6	483	10	Q9EXX0	homo sapien
44	397	17.6	483	10	Q9EXX0	homo sapien
45	385	17.1	500	5	Q9EXX0	homo sapien
46	385	17.1	500	5	Q9EXX0	homo sapien
47	370	16.4	539	11	Q9EXX0	homo sapien
48	367	16.3	510	11	Q9EXX0	homo sapien
49	367	16.3	510	11	Q9EXX0	homo sapien

ALIGNMENTS

RESULT 1

Q9EXX0 ID Q9EXX0 PRELIMINARY: PRT: 428 AA.

AC Q9EXX0: 2001 (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)

DE Pcpn proto-oncogene protein.

OS Homo sapiens

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606,

XP SEQUENCE FROM N.A.

RA MEDLINE=20173601, PubMed=10708485;

RA Racio J.A., Zambano N., Pense, Ld, Reig J.A., Rhoads A., Rouzaut A.,

RT "The human Pcpn proto-oncogene: cDNA identification, primary

RT structure, chromosomal mapping, and expression in normal and tumor

RT cells";

RT ENZY: 37393-236 (2000).

DR ENZY: 37393-236 (2000).

DR InterPro: IPR000407; GDAI_C039_NTPase.

DR Pfam: PF01150; GDAI_C039_NTPase.

SQ SEQUENCE 428 AA; 47431 MW; F2CAF705E044F6 CRC64;

Query Match

Best Local Similarity 99.4%; Score 2236; DB 4; Length 428;

Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MATHSGTFFVFLVVCVCSNHHNNQNTQEGIFLSSNCPINVSASTLYGIMFQASGTGT 60

1 MATHSGTFFVFLVVCVCSNHHNNQNTQEGIFLSSNCPINVSASTLYGIMFQASGTGT 60

Oy 61 RHVYTFVQKQPLPLEEVEFVSFKGLSAPVQPKQKQETVOGLLEKANDKISFRSH 120

61 RHVYTFVQKQPLPLEEVEFVSFKGLSAPVQPKQKQETVOGLLEKANDKISFRSH 120

Db 61 RHVYTFVQKQPLPLEEVEFVSFKGLSAPVQPKQKQETVOGLLEKANDKISFRSH 120

Oy 121 KTVPLVKATGLLEPEKAKALLFEVKEIPKSPFLVPGVSVISMGSDGELAVTV 180

121 KTVPLVKATGLLEPEKAKALLFEVKEIPKSPFLVPGVSVISMGSDGELAVTV 180

Db 121 KPTPVKATAGLRLPEHKAALPEVMEIFKRSFPLVPGKSVNSINQSDGGLANVTY 180
QY 181 NPTUQHQHQBQVTVGLDLAGASTQITFLPEKTLKQVLPGLTSPFNWSTYKLYTH 240
Db 181 NPTUQHQHQBQVTVGLDLAGASTQITFLPEKTLKQVLPGLTSPFNWSTYKLYTH 240
QY 241 SYLGGFKAAALATLGALETSTQDGTFRSACLPRMELKWIPOGVYVQGNQGEVGF 300
Db 241 SYLGGFKAAALATLGALETSTQDGTFRSACLPRMELKWIPOGVYVQGNQGEVGF 300
QY 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 2

QMBR3 PRELIMINARY; PRT: 407 AA.
ID QMBR3
AC STRAIN-C57BL/6J; TISSUE:Testis;
DB 01-MAR-2002 (TMBLrel. 20, Created)
DT 01-MAR-2002 (TMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TMBLrel. 23, Last annotation update)
DS Mus musculus (Mouse)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN (1) NC_014968;
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE:Colon;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL, BC020966; AAR0966.1; -;
DR InterPro; IPR000407; GDAI_C039_WTPASE.
KW Hydrolase; (1) GDAI_C039; 1.
SQ SEQUENCE 407 AA, 45336 Wt, D925PTDCRCE5B CRC44;

Query Match 92.58; Score 2104; DB 4; Length 407;
Best Local Similarity 100.0; Pred. No. 8.7e-174; Caps 0;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSNGTVFPMILVUSVCVANSRQNTWFERGIFLSKWCPIVNSASTLYGVMPDAGSTGT 60
Db 1 MATSNGTVFPMILVUSVCVANSRQNTWFERGIFLSKWCPIVNSASTLYGVMPDAGSTGT 60
QY 61 RIHYVTVFVQNGQLPLLEGVTSKQSLAFVQKQKQASTVOGLLEVAKDSIFRSH 120
Db 61 RIHYVTVFVQNGQLPLLEGVTSKQSLAFVQKQKQASTVOGLLEVAKDSIFRSH 120
QY 61 RIHYVTVFVQNGQLPLLEGVTSKQSLAFVQKQKQASTVOGLLEVAKDSIFRSH 120
Db 61 RIHYVTVFVQNGQLPLLEGVTSKQSLAFVQKQKQASTVOGLLEVAKDSIFRSH 120
QY 121 KWTQVPLKATQKQLPEHKAALPEVMEIFKRSFPLVPGKSVNSINQSDGGLANVTY 180
Db 121 KWTQVPLKATQKQLPEHKAALPEVMEIFKRSFPLVPGKSVNSINQSDGGLANVTY 180
QY 181 NPTUQHQHQBQVTVGLDLAGASTQITFLPEKTLKQVLPGLTSPFNWSTYKLYTH 240
Db 181 NPTUQHQHQBQVTVGLDLAGASTQITFLPEKTLKQVLPGLTSPFNWSTYKLYTH 240
QY 241 SYLGGFKAAALATLGALETSTQDGTFRSACLPRMELKWIPOGVYVQGNQGEVGF 300
Db 241 SYLGGFKAAALATLGALETSTQDGTFRSACLPRMELKWIPOGVYVQGNQGEVGF 300
QY 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 4

QMBR23 PRELIMINARY; PRT: 437 AA.
ID QMBR23
AC STRAIN-C57BL/6J; TISSUE:Testis;
DB 01-MAR-2003 (TMBLrel. 23, Created)

Db 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 3

QMBR23 PRELIMINARY; PRT: 427 AA.
ID QMBR23
AC STRAIN-C57BL/6J; TISSUE:Testis;
DB 01-MAR-2003 (TMBLrel. 23, Created)
DT 01-MAR-2003 (TMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TMBLrel. 23, Last annotation update)
DS Mus musculus (Mouse)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Murinae; Mus.
RN (1) NC_014968;
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE:Testis;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL, BC020966; AAR0966.1; -;
DR InterPro; IPR000407; GDAI_C039_WTPASE.
KW Hydrolase; (1) GDAI_C039; 1.
SQ SEQUENCE 427 AA, 47101 Wt, 6E3773C942B58477 CRC64;

Query Match 88.58; Score 1990.5; DB 11; Length 427;
Best Local Similarity 88.18; Pred. No. 6.5e-164;
Matches 376; Conservative 25; Mismatches 25; Indels 1; Gaps 1;
QY 1 MATSNGTVFPMILVUSVCVANSRQNTWFERGIFLSKWCPIVNSASTLYGVMPDAGSTGT 60
Db 1 MATSNGTVFPMILVUSVCVANSRQNTWFERGIFLSKWCPIVNSASTLYGVMPDAGSTGT 60
QY 61 RIHYVTVFVQNGQLPLLEGVTSKQSLAFVQKQKQASTVOGLLEVAKDSIFRSH 120
Db 61 RIHYVTVFVQNGQLPLLEGVTSKQSLAFVQKQKQASTVOGLLEVAKDSIFRSH 120
QY 121 KWTQVPLKATQKQLPEHKAALPEVMEIFKRSFPLVPGKSVNSINQSDGGLANVTY 180
Db 121 KWTQVPLKATQKQLPEHKAALPEVMEIFKRSFPLVPGKSVNSINQSDGGLANVTY 180
QY 181 NPTUQHQHQBQVTVGLDLAGASTQITFLPEKTLKQVLPGLTSPFNWSTYKLYTH 240
Db 181 NPTUQHQHQBQVTVGLDLAGASTQITFLPEKTLKQVLPGLTSPFNWSTYKLYTH 240
QY 241 SYLGGFKAAALATLGALETSTQDGTFRSACLPRMELKWIPOGVYVQGNQGEVGF 300
Db 241 SYLGGFKAAALATLGALETSTQDGTFRSACLPRMELKWIPOGVYVQGNQGEVGF 300
QY 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 301 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
Db 361 EPCYAVLRVWRKQHPQEVQSGFVAFYSYVDRADVTDWIDYKGGILKVEDFERKAR 360
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

295 KF-WINGSDGSTRHIVYTFVQKPGQPLIEGVFDSVKSGLSAFVQKPGQASTVOGLL 353
 Db AC 01-MAR-2003 (TREMblrel. 23, Created)
 Qy 346 KGLTGLAVDFEFKAREVC-----DLNLETSGAGPLDMLSVITALLKQGFAGTAVLOL 401
 Db DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 Db 354 EGGELQAFKAEABICAREKTEIDDSGHWPFQGLQMLTIVSLKQGVFEDNPLVL 413
 Qy 402 TKKNNITFTWGLQATF 418
 Db 414 AKIKGKGVQGLAF 430

RESULT 10
 QCH23 PRELIMINARY; PRT; 276 AA.
 AC 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Putative quinosine-diphosphatase 6.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 MN 13_TaxID=10090;
 NC 13_TaxID=10090;
 RN 13_TaxID=10090;
 RP Schizosaccharomyces pombe.
 RC STRAIN=C57BL/6J; Tissue=Mammary gland;
 RA Straubinger et al. (1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC038126; AHI39126.1.
 DR Hydrolyase.
 KW Hydrolyase.
 SQ SEQUENCE 276 AA; 3010 MW; 75A92DDIAC7629TF CRC64;

Query Match 26.48; Score 593; DB 11; Length 278;
 Best Local Similarity 56.04; Pred. No. 4.9e-43;
 Matches 119; Conservative 31; Mismatches 49; Indels 6; Gaps 2;

Qy 49 YGIMFDAGSTGRHIVYTFVQKPGQPLIEGVFDSVKSGLSAFVQKPGQASTVOGLL 108
 Db 74 YGIMFDAGSTGRHIVYTFVQKPGQPLIEGVFDSVKSGLSAFVQKPGQASTVOGLL 132
 Qy 109 EVAKDSIPRSHKHKTIVVLTATGRLLPKHAALFVFKSIFPKVPGKVSIMD 168
 Db 123 NVAKGSIYFPMATKATGRLLPKHAALFVFKSIFPKVPGKVSIMD 192
 Qy 169 GDSGLTAVNFTLQMLQHOHRTVGTLDLGGASTVTFPQKTLCTPGVLTFS 228
 Db 193 OTGKVSAMITVNSGLKTPGSSVGNMLDGGSTVTLFVSTQVIGASFGHIAL 252
 Qy 229 INFNTYKLTHTSYGLGKLA 253
 Db 253 QNRYNTLYKLTSTRW-----CSRLA 272

RESULT 11
 QCH23 PRELIMINARY; PRT; 556 AA.
 AC 01-MAR-2003 (TREMblrel. 13, Created)
 DT 01-MAR-2003 (TREMblrel. 13, Last sequence update)
 DE Putative quinosine-diphosphatase (guanosine diphosphatase).
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 MN 13_TaxID=10090;
 NC 13_TaxID=10090;
 RN 13_TaxID=10090;
 RP Schizosaccharomyces pombe (Fission yeast).
 RC Straubinger et al. (1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC038126; AHI39126.1.
 DR Hydrolyase.
 KW Hydrolyase.
 SQ SEQUENCE FROM N.A.
 RC STRAIN=B972h-1;
 RA Barrett B.G.; Rajandream M.A.; Quail M.; Seagar K.; Harris D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN 12

RP Schizosaccharomyces pombe.
 RC Straubinger et al. (1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC038126; AHI39126.1.
 DR Hydrolyase.
 KW Hydrolyase.
 SQ SEQUENCE 556 AA; 6158 MW; 1D81E3D6A8BB85 CRC64;

Query Match 23.91; Score 538.5; DB 3; Length 556;
 Best Local Similarity 56.04; Pred. No. 4.9e-43;
 Matches 144; Conservative 61; Mismatches 157; Indels 57; Gaps 13;

Qy 49 YGIMFDAGSTGRHIVYTFVQKPGQPLIEGVFDSVKSGLSAFVQKPGQASTVOGLL 108
 Db 134 YGIMFDAGSTGRHIVYTFVQKPGQPLIEGVFDSVKSGLSAFVQKPGQASTVOGLL 191
 Qy 109 EVAKDSIPRSHKHKTIVVLTATGRLLPKHAALFVFKSIFPKVPGKVSIMD 168
 Db 123 NVAKGSIYFPMATKATGRLLPKHAALFVFKSIFPKVPGKVSIMD 192
 Qy 169 GDSGLTAVNFTLQMLQHOHRTVGTLDLGGASTVTFPQKTLCTPGVLTFS 228
 Db 193 OTGKVSAMITVNSGLKTPGSSVGNMLDGGSTVTLFVSTQVIGASFGHIAL 252
 Qy 229 INFNTYKLTHTSYGLGKLA 253
 Db 253 QNRYNTLYKLTSTRW-----CSRLA 272

RESULT 12
 QCH23 PRELIMINARY; PRT; 489 AA.
 AC 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DE Putative pyrase.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 MN 13_TaxID=10090;
 NC 13_TaxID=10090;
 RN 13_TaxID=10090;
 RP Schizosaccharomyces pombe (Fission yeast).
 RC Straubinger et al. (1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC038126; AHI39126.1.
 DR Hydrolyase.
 KW Hydrolyase.
 SQ SEQUENCE FROM N.A.
 RC STRAIN=B972h-1;
 RA Barrett B.G.; Rajandream M.A.; Quail M.; Seagar K.; Harris D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN 12

Query Match 23.04; Score 518.5; DB 10; Length 489;
 Best Local Similarity 56.04; Pred. No. 3.4e-36;
 Matches 143; Conservative 70; Mismatches 149; Indels 59; Gaps 16;

Qy 309 RVWGLHJLQREY-----QSGSEAFVAFYVAVDTMDIVKSGI---LKVDEPKARE 361
 Db 389 -----NCHQPSLHFFFAETSDYVAFYDFT-----QPLGLPFLSTLOELQALRT 436
 Qy 362 VCDMLNFTS-----QS-----PFLQWLSYVTLAKGQFPAUSFVQLKRWYNI 408
 Db 437 VNGEIVESVFGESGSELSEKFEQWCLDNLVQSLHTGVDIPQRELRATKIANN 496
 Qy 409 ETWALGNATHLOS 423
 Db 497 ELONGASLPLSS 511

RESULT 15
 Q9SPW% PRELIMINARY: PRT: 455 AA.

ID Q9SPM6 (TREMREL 13, Created)
 AC 01-MAR-2000 (TREMREL 13, Last sequence update)
 DT 01-MAY-2000 (TREMREL 13, Last sequence update)
 DT 01-MAR-2002 (TREMREL 20, Last annotation update)
 DE Nod factor binding lectin-nucleotide phosphohydrolase.
 OS Medicago sativa (alfalfa).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 CC Eurosidia 1; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 SN [1]_Xenid3877,
 SN SEQUENCE FROM N.A.

RP YISUERROOT;1909; PubMed-10517321.
 RC Robert N.J., Brigham J., Wu B., Murphy J.B., Volpin H.,
 EA Phillips D.A., Etzler N.E.;
 ET "A nod factor-binding lectin is a member of a distinct class of
 RL nod factor-binding lectins in the legumes." ;
 RL Mol. Gen. Genet. 262:261-267(1999).
 DR EMBL: AF156782; AAF00611.1;
 DR InterPro: IPR000407; G04; C035_NTPase.
 DR Gene: 128000; Medicago sativa; Medicago sativa; Medicago
 DR PROSITE: PS01238; G041_C035_NTPASE; 1.
 KW Hydrolase; Lectin.

Qy SEQUENCE 455 AA; 49879 MW; 69122846D7EC261B CRC64;
 Query Match 22.6%; Score 507.5; DB 10; Length 455;
 Best Local Similarity 34.0%; Pred. No. 2.7e-35;
 Matches 143; Conservative 65; Mismatches 152; Indels 61; Gaps 16;

Qy 47 TLVGIWPDAGSTGRHIVTVQKMFQPLPIL-----SGEVFVRVPGLSAFVQVQKNE 102
 Db 43 TSIAVTFDAGSTGRHIVTVQKMFQPLPIL-----NLLLRHGMIDFVQKIFGLSAYGNPQAAK 98
 Qy 103 TWQGLVAVAGSIPSHMKTPVVLKATAGLLPEKAKALLFVEIF-RKSPFLVPK 161
 Db 99 SLTILEAEDVPEDLHFKTPKPLRIGTAGLLNGDAEKILQATRNFRNSRLNVR 158
 Qy 162 GSVISMGSDICLAWTNELTQSLGHROETVGTGLDGAOSTQTFPLPQEKLEQPT 221
 Db 159 DAVSITDQCSQWMTVNTVGNLGSFKTSKVGVIDGSGVQMTYAVS-KTIAANP 217
 Qy 222 R-----GYLTSEPMNSTYKLVTHSYGFLKGLAKLATLGALETGDTGHTFSACLPR 275
 Db 218 KVAGSDPYIKLVKKGQYOLYVHSYLFKGEATQAVUNA--TNGS-----ANFCLIF 270
 Qy 276 WLEAEIMFGCVTVQGVQSGVEGFECVAVLVVTRCKLHQPEVQSGP----- 326
 Db 271 GFNGTTFSTGVYAFAPFSGSS-NPDDCKEILKVL--KVMECFVPSCTFGIWNQGGG 327
 Qy 327 -----VAEYTYDRAVDTMDIVKYG-GLIKVDFEPEKARVCD-MLNFTS---- 371
 Db 328 SQCKALFTSAENTL--AEDVGWVEKPNPSILHPVFEIEMKACALNFDVKSTYPR 384
 Qy 372 ---GSPFLQGLSYITALLQGFQFA---DSTVLQJLKQNN-ITGHALGNATHLOS 423

Db 385 ITDAGRPVYCHOLLQVLLVHGQLOPFRKLTITVGGSTQVQNSVDEAWPLQTVNVAISA 444
 Qy 424 L 424
 Db 445 L 445

Search completed: November 13, 2003, 06:19:43
 Job time : 63 secs

[illegible]

RESULT 6
 Probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
 CSpecies: Arabidopsis thaliana (mouse-eat cross)
 CAccession: G84442 #sequence_revision 02-Feb-20001 Next_change 18-Nov-2002
 CAccession: G84442
 CRef: Rabin, J.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beittlo, M.I.; Town, C.D.; Fujiki, C.Y.;
 Kim, R.O.; Moffatt, K.; Cronin, L.A.; Shen, W.; Mankens, S.E.; Maynard, J.; Tallon, B.;
 Nelson, D.; Nelson, G.; Rhee, S.A.; Saltsz, S.L.; Fraser, C.N.; Venturi, A.
 Nature 402, 761-768, 1999
 CTitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 CAccession: A04420 and NID:20053487; RND10617157
 A:Accession: G84442
 A:Status: preliminary
 A:Species: Arabidopsis thaliana
 A:Residues: 1516 CDS
 A:Cross-references: GR:AE020293; NID:G3461821; PDB:1AC32915.1. GSDB:G800139
 A:GeneID: 2002970
 A:Map position: 2
 C:Superfamily: nucleoside triphosphatase chromatin-associated
 Best Watch 18.9% Score 425.5 DB 2 Length 516;
 Query Local Similarity 30.6% Prd. No. 1.5e-27
 Matches 12; Conservative 61; Mismatch 159; Indels 73; Gaps 13;
 42 NVASATLGVGIMDAGSTGTRHYVTFVQWQKQFLTLR-GEVFSQVYK-PGLSAGVDP 97

152 VRSGLNYPF--PQGARLTIOBEGAYGWTITNLLGNFKGQKTFMSI VPIETNRQET 209
 QY
 Db 196 GTDLGAGNSTQITLPPCEKTLTQPTGTVTSPFSTYKLTHTSLGKGLKAAALATL 255
 Db 210 GALLDGLGASGVTVFVDP--NOTIE--SPONAL--OPRLYKGVYVTHSLFLCYGKQAL--WOML 266
 QY 256 GALTGTGTGHTSACLL-----PRLBENWIFGVGVYGVGNORSE 297
 Db 267 GQGVQVANSLEILDPCEPHQYKVVNVSDLYKTHCTCTCFEMTLFQFQELQGN-- 321
 QY 298 VQGFPEFVANSVLEW-----VRGLKQDEVEVSGFVASYVYDRAVDWIDME 345
 322 --YQCHQSLLEFNTSYCPVQCANFHPLEPLQIQFGFSAP--YFNKFLN---URSE 375
 QY 346 KQGLTAVDFPER--ARVCONLENFTSG--SPEL---CHULSYTALLKQGEF--ADS-T 397
 Db 376 KYSGKEVTKMKKFCQAPRKEIKTSYAVKXVLYSCFSTGTHLSLLOOYHFTDME 435
 QY 398 YLQYKVNINICTGALGATFHL 420
 Db 436 HNFPTKIOESDAGTGLGMINL 458
 RESULT 12
 T04856
 Probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
 CDate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 CAccession: T04856
 R:Raspberger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrall, B.G.
 A:Reference: 1998
 A:Reference: 2000
 A:Reference: 2002
 A:Accession: T04856
 A:Status: preliminary; translated from GB/EMLL/DB04
 A:Species: Yeast
 A:Accession: T04856
 A:Experimental source: EMBL:AL121783; PIDN:CA857841.1; SPDB:SPFC11810.05c
 A:Cross-references: EMBL:AL121783; PIDN:CA857841.1; SPDB:GN00068; SPDB:SPFC11810.05c
 A:Gene: SPDB:SPFC11810.05c
 A:Map position: 3

Query Match 15.41; Score 347; Db 2; Length 572;
 Best Local Similarity 25.51; Pred. No. 6,620; 11;
 Matches 115; Conservative 67; Mismatches 151; Indels 112; Gaps 16;
 QY 49 YCMFDRAGSTRIHVTFF-----VQVMQQLPILEGVDP-----SVKRLAVDP 95
 Db 5 YGIFDAGSGSRLILYSDMDTDSLSDDVKVLPILFTGIDGGKWSLKVGQISFEN 64
 QY 96 QATVQGLLEAVKDSIPSHKWKTVLAKRILL--PEKAKALLFVEKFER 153
 Db 65 NPGKWSKLELLDPAANLAPKPVKSTFTVPSATNRRLLGVQANLASHACRYIK 124
 QY 154 KSPFLPV--KGSVSHQSDGLLAWYVWFLQGLHQRGTQVTDLDGASQTITLP 211
 Db 125 NTFDIPKNSNIRVDGAKBGMWGLATYLLTLEKSTQSTVQPLDGGASVQIAL-- 182
 QY 212 OFEKTILTPGRTYSFEMST-----PKLTHSYLGRCAARLALQAL-- 258
 Db 183 -----ELFSPQLNKKSLSTVHGLQNGQQLYELFTVTLQFNGAVNAYVGLLL 235
 QY 259 ETE--GTGHTFSAFLPRLBENWIFGVYKVGQ-----NORGEVGFECY 304
 Db 236 ESENGKVNITLSDPCLSL--GRYTDIGIEFAGTGQKQKQLKTLNLLNPKCSNOC 293
 QY 305 ABVLRVVGLKGLQPREVGSGFVASYVYDRAVDWIDMEKGLKVEDPERNAEVC-- 363
 Db 294 FQGLT-----PPVDFANTFVFGSEFWTTNVD-----FNGSGVYFNFYKVEYCO 343
 QY 364 -----DLNRTSPSSPFLCHDLSYITALKLQKGFADSTY----- 398
 Db 344.TBWKTHLSLYNELKLTSTSDNLK-----LTPKASVALVLRHSDVPKNTSSND 396

399 -----LQTKYNNINICTALG 415
 Db 397 AKDGLSVTPAYSPFSTLEKTERTEVNTVLG 427
 RESULT 13
 E86276
 Hypothetical protein F147L7.1 - Arabidopsis thaliana
 CDate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 CAccession: E86276
 R:Rheologis, A.; Becker, J.R.; Palm, C.J.; Pedersen, N.A.; Kaul, S.; White, O.; Alonso
 Chn. N.P.; Hudson, M.L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dwyer, R.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Rhykin, E.; Kim,
 C.A.; Li, J.H.; Li, T.; Lin, D.; Liu, Z.A.; Luo, J.S.; Marti, R.; Mazzali,
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Kar, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Accession: E86276
 A:Status: preliminary
 A:Molecule type: DNA
 A:Cross-references: GB:AE005172; NID:G7262666; PIDN:NAF43324.1; GSPDB:GN00141
 A:Gene: E86276
 A:Map position: 1

Query Match 14.64; Score 329.5; Db 2; Length 405;
 Best Local Similarity 26.33; Pred. No. 1,2e+19;
 Matches 110; Conservative 63; Mismatches 158; Indels 97; Gaps 15;
 QY 48 LYCMFDRAGSTRIHVTFFVQVMQQLPILEGVDFSVKGLSAPVDQPKGAGTVOCL 107
 Db 3 VGVWYFSESKP-----VDFQGEHYASL-----KLSPGLSYADNPBGASVSTKL 48
 QY 108 LEVAKDSIPSHKWKTVLAKRILLPEKAKALLFVEKFERPKSPFLVPGKSVSTM 167
 Db 49 VEPKGRIPKGLKESDILRNATAMRLLDVQVQEGILDVTFVRSQSGFKQGMATV 108
 QY 160 DGGEGDGLAWYVWFLQGLHQRGTQVTDLDGASQTITLTPLEKTLTPQRLGTS 227
 Db 109 AGTDGTYANVAVNHALSLGQDLPKTTGIVELGASAGATTFVS-----BNVPFEST 163
 QY 228 FPMNYSYLYKLYGLQGLAKRLATLCAETE-----GTGHTFSAFLP 275
 Db 164 ISYGNYSYLYSHSFDLQDPADEKLSLSQNSVAASDGDGVDPKGYVTDNHSQ 223
 QY 276 -----KLEAKNP--GVYQVGVGNQSGVGFPCVAVLTVR--GKHLQPREVQGSFYA 328
 Db 224 XGSSFLSEESKFASCAVQAASG-----FTKRSNTANLQNGEN----- 265
 QY 329 SYVDRADVDWIDMEKGLKVEDPERNAEVC-----EYKAVCDNL 366
 Db 266 --CYVHCHGSGITFTNPKGSLFATENFTFTKFGSEKWSLNLAKGFCGSEWSKL 324
 QY 367 ENP--TSGSPFL--CHULSYTALLKQGEF--ADS-TVQLQVY--NNTFQWALCA 416
 Db 325 XENYPTTKYVNFYSFASVYLSMLHSDGLVALDERIKYASKAKENIPLQWALCA 382

RESULT 14
 T04439
 Hypothetical protein T18816.150 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 CDate: 02-Mar-2001 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 CAccession: T04439
 R:Bevan, M.; Bancroft, I.; Reimann, S.; Jorkova, M.; Anzorge, M.; Bancroft, I.; Mowes, H.
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: 215359

A:Accession: T04439
 A:Molecule type: DNA
 A:Residues: 1-1052 (REV)
 A:Cross-references: EMBL:AL021497
 C:Genetic: clonal source: Cultivar Columbia; BAC clone T1816
 A:Map position: 4
 A:Introns: 79/3; 118/3; 217/3; 295/3; 396/3; 531/2; 815/3
 A:Note: T1816.150

Query Match 12.21; Score 274; DB 2; Length 1052;
 Best Local Similarity 24.99; Pred. No. 2.1e-14;
 Matches 107; Conservative 70; Mismatches 171; Indels 82; Gaps 19;

QY 51 INFAGDSGTIRHVV--TVQMGKPGQGLPIL-----ECVFPD--SVKGLSAFV 94
 DB 525 LVIYVSTGTRAVVAVSVINFGSSDITVWMSITGELSKRSHKADMETEPDRLV 584
 QY 94 DQPOQAEI--VOGLLVANDIIPRSHWKTTPVLKATAGLALPEHKAALLFEVEIFR 153
 DB 545 NN--TKLTKLPELQWAKIKIPKSHARTSLFVYATGATVGRPADSSMILGNW51A 643
 QY 154 KPPFLVPKGSVIMQSDGDLAAVYVNFVLTQQLHQ--HQSTVGTLDGGAGTQITLQ 212
 DB 644 KPTPTCRWKKIISGTEATFQWALVYVNTSGNLGAPGATFALDGGSLQVFPME 703
 QY 213 FENLTQTPROVITSEFMENSTVYLYSTLSTGLKAA-----RLATL----- 255
 DB 704 -ERTHEYN-----LHAKGVVHHLGATSLAGLQGLADQAFVSHLLKLPVNMKDI 758
 QY 256 GALTETGTPHTRFACLEPRLKLEIMFGGVVQVQGNQGEVGEF-----PCYAEVR 309
 DB 759 GKLE-----MEHPCLANGSNQGYICSOCAVSGGKNGKGVSHVGLPWNQCEA 310
 QY 310 VVR--GKLRHQPVEVQR--GSFVAFSVYORAVITMDVEXGIL--LKVEDFERKARVC 363
 DB 811 LAKWAPCKLPOTPRAPQPTAVSGFF-----VYFRFNLSAASLDVLEKRGFC 862
 QY 364 DN-----LENTSSGSPFL--CHULSVITLAKNGCFADSTV-----LQITKYWNIE 410
 DB 863 DKAQVAVSVSGPFFEDYCFRAPHVLSLRREGLYITDQKIIIGSGSITWTLGVALLES 922
 QY 411 GAWNGKTHL 420
 DB 923 GKALSTLGL 932

RESULT 15
 C86276
 C:Source: protein - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (necrose ear cross)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Nov-2002
 C:Accession: C86276
 R:Biologists: Chong, W.K., Combs, J.E., Conner, A.H., Crou, J.H., Dowd, R.,
 Hansen, N.F., Hughes, B., Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Klaykin, E.; Kim, C.
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Klaykin, E.; Kim, C.;
 A:Authors: Salzborg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 A:Authors: Salzborg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 A:Authors: Salzborg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 A:Authors: Salzborg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 A:Reference number: A86141; PMID:21016739; PMID:11130712
 A:Accession: C86276
 A:Status: Preliminary
 A:Map position: 1
 A:Residues: 1-508 (REV)
 A:Cross-references: GB:AE05172; NID:G5080800; PID:AA039310.1; GSPDB:GN00141
 C:Genetics:
 C:Map position: 1
 C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 11.01; Score 248; DB 2; Length 508;
 Best Local Similarity 23.38; Pred. No. 1.1e-12;
 Matches 110; Conservative 77; Mismatches 159; Indels 126; Gaps 21;

QY 12 LVVSCISGVV-----SHRNOCPWFQFLSMCHINWASTLGIWFDAGSTGT 60
 DB 35 VIVACVITAGLGLFGYSLASGRNR-----VSLHVSVIDGSSGT 77
 QY 63 KINVPFVQVQGELEL--GEVDSYK--QLSASFQPKQAGATVOGLIVANDISF 116
 DB 79 AVHVGV--RISSCKVFDGEENTVAELKLSFQLSAVADNPFQGVSESVTELVFAKRVH 135
 QY 117 ESHKQVTVKATAGLLEPHKALFEVKEIKESKLPVPSKVSIMQSDG--GI 174
 DB 136 KGLKMSDILKATAMHLLPEQVGLDVTREVRLESCF-----DPRCWASV 185
 QY 175 LAMVTVFGGLGKQFETVGTLDG-----GASTQITLPOEVTLEOTPRGLYLSF 228
 DB 186 IESTLENF-----QDLKVMHLLALLNREVRLEVFY-----STELVSEFRTL 231
 QY 229 EHSNYSKLVSTLQFSLKKAARLALGAL-----FTTGCTGHTFRGALVWLEAWI 282
 DB 232 AYGVNYSVLNLSLFDQDAQAEKLSBELVNSAANSTGRIVPDCCIPKGYLETNQLK 325
 QY 283 --PGVYGVQVGNQGEVQPERYAVLVRVVR-----GKLRHQPVEVQGS 325
 DB 292 DLGFGKLDKQKFTALQAGNFSEGRSAFAMLGEENKAKCTVETSGISGTFITN--LQGS 349
 QY 326 FYVSYFY-----DRAVTDVI-----DYKQGLIYNEDFERKAREVQDME 367
 DB 350 FLATENFHTSFFGLGEKLEMLSLAKRKFCEEMSK--LAKVYPTFKD---ENLL 402
 QY 368 NHTSGFFLCHDLSITALLKQGFQFA-DSTVLQITKIV--NHTETGALCA 416
 DB 403 KY-----CFSSXILLNLSHLSLAVALDESIKYASAGEDIPLDVALCA 447

Search completed: November 13, 2003, 06:20:21
 Job time : 54 secs


```

Query Match      100.0%; Score 2250; DB 12; Length 428;
Basic Local Similarity 100.0%; Pred. No. 1.5e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATSNGTFFMLVSCVCAVSHRNQOVTVEGIFLSKCFINVASLTGIMFDAGSTGT 60
Db 1 MATSNGTFFMLVSCVCAVSHRNQOVTVEGIFLSKCFINVASLTGIMFDAGSTGT 60

Qy 61 RHIVVTFVQMGQGLPILEGVEFVSFKGSAFYDQKQAGTVOQLLEVAKOSTPRSH 120
Db 61 RHIVVTFVQMGQGLPILEGVEFVSFKGSAFYDQKQAGTVOQLLEVAKOSTPRSH 120

Qy 121 KKTPTVLAATAGLALPEHKAKALFEVKEFRKSPFLPKVKSVMGSGDEGILAWTV 180
Db 121 KKTPTVLAATAGLALPEHKAKALFEVKEFRKSPFLPKVKSVMGSGDEGILAWTV 180

Qy 181 NFTUQGHQRTVGTLDGASQVITLQPKETLSQTFRGVLSFEMFNSTYLYTH 240
Db 181 NFTUQGHQRTVGTLDGASQVITLQPKETLSQTFRGVLSFEMFNSTYLYTH 240

Qy 241 SYLGGLAAKALATLGALETGDTGHTFSACLPRLBAEMI FGQVYQVGNQGEVGF 300
Db 241 SYLGGLAAKALATLGALETGDTGHTFSACLPRLBAEMI FGQVYQVGNQGEVGF 300

Qy 301 ECTAEVLRVKGKQDEVOFGVSFYAFSTYDRAVDTMDIVKGLKAVDFPERAK 360
Db 301 ECTAEVLRVKGKQDEVOFGVSFYAFSTYDRAVDTMDIVKGLKAVDFPERAK 360

Qy 361 EVCNLENTSGSPFLCNDLSYITALLKDGSGFADSVLQTKKXNMIFTCWALGATFL 420
Db 361 EVCNLENTSGSPFLCNDLSYITALLKDGSGFADSVLQTKKXNMIFTCWALGATFL 420

Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 3
US-10-091-085-3
Publication No. US20030175752A1
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36457CON
CURRENT FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1998-07-16
PRIORITY APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1995-08-09
PRIORITY APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1995-07-16
PRIORITY APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1995-03-13
PRIORITY APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
PRIORITY APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1995-07-16
PRIORITY APPLICATION NUMBER: 05/244,444
PRIOR FILING DATE: 1995-02-04
SOFTWARE: SEQ ID NOS: 23
SEQ ID NO 3
LENGTH: 428
CONSERVATION:
US-10-091-085-3

Query Match      100.0%; Score 2250; DB 14; Length 428;
Basic Local Similarity 100.0%; Pred. No. 1.5e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATSNGTFFMLVSCVCAVSHRNQOVTVEGIFLSKCFINVASLTGIMFDAGSTGT 60
Db 1 MATSNGTFFMLVSCVCAVSHRNQOVTVEGIFLSKCFINVASLTGIMFDAGSTGT 60

Qy 61 RHIVVTFVQMGQGLPILEGVEFVSFKGSAFYDQKQAGTVOQLLEVAKOSTPRSH 120
Db 61 RHIVVTFVQMGQGLPILEGVEFVSFKGSAFYDQKQAGTVOQLLEVAKOSTPRSH 120

Qy 121 KKTPTVLAATAGLALPEHKAKALFEVKEFRKSPFLPKVKSVMGSGDEGILAWTV 180
Db 121 KKTPTVLAATAGLALPEHKAKALFEVKEFRKSPFLPKVKSVMGSGDEGILAWTV 180

Qy 181 NFTUQGHQRTVGTLDGASQVITLQPKETLSQTFRGVLSFEMFNSTYLYTH 240
Db 181 NFTUQGHQRTVGTLDGASQVITLQPKETLSQTFRGVLSFEMFNSTYLYTH 240

Qy 241 SYLGGLAAKALATLGALETGDTGHTFSACLPRLBAEMI FGQVYQVGNQGEVGF 300
Db 241 SYLGGLAAKALATLGALETGDTGHTFSACLPRLBAEMI FGQVYQVGNQGEVGF 300

Qy 301 ECTAEVLRVKGKQDEVOFGVSFYAFSTYDRAVDTMDIVKGLKAVDFPERAK 360
Db 301 ECTAEVLRVKGKQDEVOFGVSFYAFSTYDRAVDTMDIVKGLKAVDFPERAK 360

Qy 361 EVCNLENTSGSPFLCNDLSYITALLKDGSGFADSVLQTKKXNMIFTCWALGATFL 420
Db 361 EVCNLENTSGSPFLCNDLSYITALLKDGSGFADSVLQTKKXNMIFTCWALGATFL 420

Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

SEQUENCE 3
US-10-284-926-5
Sequence 5, Application US/10286926
Publication No. US20030175752A1
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36457CON
CURRENT APPLICATION NUMBER: US/10/286,926
PRIORITY APPLICATION NUMBER: 09/257,000
PRIOR FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1998-07-16
PRIORITY APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1995-08-09
PRIORITY APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1995-07-16
PRIORITY APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1995-03-13
PRIORITY APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
PRIORITY APPLICATION NUMBER: 05/244,444
PRIOR FILING DATE: 1995-02-04
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 54
LENGTH: 428

```


121 KKTPTVATAGRLRPHKALPVEKIFRKSPLFVKGNSINMGSDGLANVTY 180
 122 KKTPTVATAGRLRPHKALPVEKIFRKSPLFVKGNSINMGSDGLANVTY 180
 181 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240
 182 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240
 183 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 184 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 241 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 242 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 243 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 301 ECTAVLVAVRQKQFVEVQSGFASFTYDRAVDTMDIKVKGILKAVDFEKAR 360
 302 ECTAVLVAVRQKQFVEVQSGFASFTYDRAVDTMDIKVKGILKAVDFEKAR 360
 361 EVDENLFTSGSFCHLSTYALKKQGFASFTYALKKQGFASFTYALKKQGFASFTY 420
 362 EVDENLFTSGSFCHLSTYALKKQGFASFTYALKKQGFASFTYALKKQGFASFTY 420
 421 LQSGISH 428
 422 LQSGISH 428

RESULT 8
 US-10-091-085-7
 ; Sequence 7, Application US/10091085
 ; Publication No. US20020146772A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; FILE REFERENCE: 28110/35761
 ; CURRENT APPLICATION NUMBER: US/10/091,085
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 428
 ; ORGANISM: Homo sapiens

Query Match 99.3%; Score 2235; DB 14; Length 428;
 Best Local Similarity 99.3%; Pred. No. 4.8e-214;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSGVTFFMLVVCVCSAVSHRQQTWFGIFLSSMCFINVSASTLYGIMFAGSTGT 60
 DB 1 MATSGVTFFMLVVCVCSAVSHRQQTWFGIFLSSMCFINVSASTLYGIMFAGSTGT 60
 QY 61 RHVYTVVQMGQQLPILEGVDFSVKGLSAFVQKQAGETVQGLLEVAKSDIPRSHW 120
 DB 61 RHVYTVVQMGQQLPILEGVDFSVKGLSAFVQKQAGETVQGLLEVAKSDIPRSHW 120
 QY 121 KKTPTVATAGRLRPHKALPVEKIFRKSPLFVKGNSINMGSDGLANVTY 180
 DB 121 KKTPTVATAGRLRPHKALPVEKIFRKSPLFVKGNSINMGSDGLANVTY 180
 QY 181 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240
 DB 181 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240

181 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240
 241 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 242 STYGRKAAARLKALETGHTFRSACLPLMEASIFGVKYGKQNGQGVGF 300
 301 ECTAVLVAVRQKQFVEVQSGFASFTYDRAVDTMDIKVKGILKAVDFEKAR 360
 302 ECTAVLVAVRQKQFVEVQSGFASFTYDRAVDTMDIKVKGILKAVDFEKAR 360
 361 EVDENLFTSGSFCHLSTYALKKQGFASFTYALKKQGFASFTYALKKQGFASFTY 420
 362 EVDENLFTSGSFCHLSTYALKKQGFASFTYALKKQGFASFTYALKKQGFASFTY 420
 421 LQSGISH 428
 422 LQSGISH 428

RESULT 9
 US-0-092-061-2
 ; Sequence 6, Application US/10092063
 ; Publication No. US20020170055A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mileo, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
 ; FILE REFERENCE: 28110/35908 US/10/092,063
 ; CURRENT APPLICATION NUMBER: 09/370,285
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: 09/99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 428
 ; ORGANISM: Homo sapiens

Query Match 99.3%; Score 2235; DB 14; Length 428;
 Best Local Similarity 99.3%; Pred. No. 4.8e-214;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSGVTFFMLVVCVCSAVSHRQQTWFGIFLSSMCFINVSASTLYGIMFAGSTGT 60
 DB 1 MATSGVTFFMLVVCVCSAVSHRQQTWFGIFLSSMCFINVSASTLYGIMFAGSTGT 60
 QY 61 RHVYTVVQMGQQLPILEGVDFSVKGLSAFVQKQAGETVQGLLEVAKSDIPRSHW 120
 DB 61 RHVYTVVQMGQQLPILEGVDFSVKGLSAFVQKQAGETVQGLLEVAKSDIPRSHW 120
 QY 121 KKTPTVATAGRLRPHKALPVEKIFRKSPLFVKGNSINMGSDGLANVTY 180
 DB 121 KKTPTVATAGRLRPHKALPVEKIFRKSPLFVKGNSINMGSDGLANVTY 180
 QY 181 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240
 DB 181 NFVQGHQHRQSTVGTLDGASQTITLPQFKLTQTRGVLTSFPMNSTYKLYTH 240

[illegible]

RESULT 10

US-10-286-926-25
 25 Application US/10286926
 Publication No. US2003017575A1
 INVENTOR: Ford, John
 APPLICANT: Ford, John
 APPLICANT: Mulero, Julio
 APPLICANT: Yeung, George
 TITLE OR INVENTION: Polysulfide
 FILE REFERENCE: 2810/36457CON
 CURRENT APPLICATION NUMBER: US/10286926
 PRIOR APPLICATION NUMBER: 05/557,800
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 05/481,238
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: 05/370,265
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: PCT/US99/16180
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: 05/50836
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: 05/73347
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: 05/122449
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 05/244444
 PRIOR APPLICATION NUMBER: 05/118,205
 PRIOR FILING DATE: 1998-07-16
 NUMBER OF SEQ ID NOS: 54
 SEQ ID NO: 1 Stemlin ver. 2.0
 SEQ ID NO: 25
 LENGTH: 405
 TYPE: PRT
 SUBMITTER: Nemo sapiens
 US-10-286-926-25

[illegible]

Db	181	NFETGLQHQBQHTVGTDLGGAGSTQITLPPKTEKLTPTGTLTSTEMFNSTLYTH	240
Qy	241	SYLGGVMAARLALGALSTGDTGHTSRACLPMEAEAMIGGVGVKGVGGVEGVG	300
Qy	241	SYLGGVMAARLALGALSTGDTGHTSRACLPMEAEAMIGGVGVKGVGGVEGVG	300
Db	241	SYLGGVMAARLALGALSTGDTGHTSRACLPMEAEAMIGGVGVKGVGGVEGVG	300
Qy	301	ECVAVRVRVKKGLDQPEEVRQGVSVFVSYTDAVDTMDEKGLVKEVFERKAR	360
Qy	301	ECVAVRVRVKKGLDQPEEVRQGVSVFVSYTDAVDTMDEKGLVKEVFERKAR	360
Db	301	ECVAVRVRVKKGLDQPEEVRQGVSVFVSYTDAVDTMDEKGLVKEVFERKAR	360
Qy	361	ECVNDLNFVGGSPFLMDLNLSTALLKKGDFGFGFPASTVLQ	400
Qy	361	ECVNDLNFVGGSPFLMDLNLSTALLKKGDFGFGFPASTVLQ	400
Qy	361	ECVNDLNFVGGSPFLMDLNLSTALLKKGDFGFGFPASTVLQ	400

RESULT 11

```

US-10-092-063-25
Publication No. US2002017005A1
PUBLICATION DATE: 1992-03-25
APPLICANT: Ford, John
APPLICANT: Muleto, Julio
TITLE OF INVENTION: METHODS
AND MATERIALS FOR
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/212,449
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/119,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SEQUENCE LISTING: Sequence ver. 2.0
SEQ ID NO 25
LENGTH: 405
TYPE: CDS
FEATURES:
    CDS(1..39)
    NAME: Homo sapiens
US-10-092-063-25

```

[illegible]

Thu Nov 13 06:30:34 2003

us-09-905-744b-6.rapb

Page 9

Search completed: November 13, 2003, 06:26:02
Job time : 45 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 06:17:36 - Search time 21 Seconds

(without alignments)
862,136 Million cell updates/sec

Title: US-09-905-744b-6

Sequence: 1 MATSNGTVFNFVWVSCVA.....ETGALGATPHALQSIGSR 428

Scoring table: BLSDM62

Gap: 10.0, Gapext 0.5

Searched: 328717 seqs, 42110958 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1. Tensid Patents db.*

2. /cm2_6/pdata/2/taa/5A COME pep.*

3. /cm2_6/pdata/2/taa/5B COME pep.*

4. /cm2_6/pdata/2/taa/6A COME pep.*

5. /cm2_6/pdata/2/taa/6B COME pep.*

6. /cm2_6/pdata/2/taa/6C COME pep.*

7. /cm2_6/pdata/2/taa/6D COME pep.*

Pred. No is the number of results predicted by chance to have a
Maximum Match of 100% and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2250	100	0	428	US-09-608-285A-5
2	2250	100	0	428	US-09-608-285A-5
3	2250	100	0	428	US-09-240-639-6
4	2250	100	0	428	US-09-240-639-9
5	2250	100	0	428	US-09-350-836B-5
6	2250	100	0	428	US-09-370-265-3
7	2250	100	0	428	US-09-370-265-5
8	2250	100	0	428	US-09-370-265-5
9	2250	100	0	428	US-09-370-265-5
10	2250	100	0	428	US-09-370-265-5
11	2233	99	3	428	US-09-608-285A-7
12	2233	99	3	428	US-09-350-836B-7
13	2233	99	3	428	US-09-370-265-7
14	2233	99	3	428	US-09-370-265-7
15	2233	99	3	428	US-09-608-285A-25
16	2104	93	5	405	US-09-370-265-25
17	2104	93	5	405	US-09-370-265-25
18	1837	81	7	428	US-09-357-800C-25
19	1837	81	7	428	US-09-357-800C-25
20	1837	81	7	428	US-09-357-800C-25
21	1837	81	7	428	US-09-357-800C-25
22	1837	81	7	428	US-09-357-800C-25
23	1837	81	7	428	US-09-357-800C-25
24	1837	81	7	428	US-09-357-800C-25
25	1837	81	7	428	US-09-357-800C-25
26	1837	81	7	428	US-09-357-800C-25
27	1837	81	7	428	US-09-357-800C-25
28	1837	81	7	428	US-09-357-800C-25
29	1837	81	7	428	US-09-357-800C-25
30	1837	81	7	428	US-09-357-800C-25
31	1837	81	7	428	US-09-357-800C-25
32	1837	81	7	428	US-09-357-800C-25
33	1837	81	7	428	US-09-357-800C-25
34	1837	81	7	428	US-09-357-800C-25
35	1837	81	7	428	US-09-357-800C-25
36	1837	81	7	428	US-09-357-800C-25
37	1837	81	7	428	US-09-357-800C-25
38	1837	81	7	428	US-09-357-800C-25
39	1837	81	7	428	US-09-357-800C-25
40	1837	81	7	428	US-09-357-800C-25
41	1837	81	7	428	US-09-357-800C-25
42	1837	81	7	428	US-09-357-800C-25
43	1837	81	7	428	US-09-357-800C-25
44	1837	81	7	428	US-09-357-800C-25
45	1837	81	7	428	US-09-357-800C-25

28	491.5	21.8	462	4	US-09-129-112-15	Sequence 15, Appl
29	485	20.8	473	4	US-09-129-112-15	Sequence 15, Appl
30	465	20.8	473	4	US-09-240-639-12	Sequence 12, Appl
31	446.5	19.8	484	4	US-09-240-639-11	Sequence 11, Appl
32	351	15.6	502	4	US-09-557-800C-55	Sequence 55, Appl
33	351	15.6	510	3	US-09-240-639-4	Sequence 4, Appl
34	342.4	15.6	510	3	US-09-240-639-4	Sequence 4, Appl
35	323.4	10.4	148	4	US-09-240-639-17	Sequence 17, Appl
36	186	8.3	153	4	US-09-240-639-13	Sequence 13, Appl
37	180.5	8.0	150	4	US-09-240-639-16	Sequence 16, Appl
38	174	7.7	154	4	US-09-240-639-14	Sequence 14, Appl
39	174	7.7	154	4	US-09-240-639-14	Sequence 14, Appl
40	106.5	4.7	553	1	US-08-565-386-12	Sequence 12, Appl
41	105.5	4.7	339	4	US-09-252-991A-20854	Sequence 20854, Appl
42	98.6	4.3	506	4	US-09-114-001C-4383	Sequence 4383, Appl
43	93	4.1	969	2	US-08-284-941-2	Sequence 2, Appl
44	93	4.1	969	2	US-08-284-941-2	Sequence 2, Appl
45	93	4.1	969	2	US-08-447-642-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-608-285A-3
Sequence 3, Application US/09608285A
Patent No. 635013
GENERAL INFORMATION:
APPLICANT: Compugen
INVENTOR: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
SEQUENCES AND THEIR USES
FILE REFERENCE: 2810/36570
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-01
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
SEQ ID NO 38
TYPE: PPT
ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match	100.0%; Score 2250; DB 4; Length 428;
Best Match Similarity	100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative	0; Mismatch 0; Indels 0; Gaps 0;
Qy	1 MATSNGTVFNFVWVSCVA...ETGALGATPHALQSIGSR 60
Db	1 MATSNGTVFNFVWVSCVA...ETGALGATPHALQSIGSR 60
Qy	61 RIIVTVQKQGLFLEGVFVSFVGLSVAFVQKGAETVQGLLEVANSIPRSHW 120

61	RHYTVYVQFQFQFQLPGESEVDFS VKGSLNPFQKQGLAETVOGLELWANDSDIPRSHM	120
121	KRTPVYATAGRLRSHKAKALLFENKTEFKRSPFLVPGVNS INQSGDQGLAVVY	180
121	KRTPVYATAGRLRSHKAKALLFENKTEFKRSPFLVPGVNS INQSGDQGLAVVY	180
181	NFTVQGLHGHQETVSTLUGAGSTQITLPEKTELEQTRCHYTSFEMNSNYVPR	240
181	NFTVQGLHGHQETVSTLUGAGSTQITLPEKTELEQTRCHYTSFEMNSNYVPR	240
241	SYLQFCAALATLQALITLQFTRFRALHLEHLEHATFOGVYVQVQSGEVE	300
241	SYLQFCAALATLQALITLQFTRFRALHLEHLEHATFOGVYVQVQSGEVE	300
301	EFCTAVYLVKVKLHQPESVQSGFVSNVKNVADLVMTVMTGKGLKPKRPSR	360
301	EFCTAVYLVKVKLHQPESVQSGFVSNVKNVADLVMTVMTGKGLKPKRPSR	360
361	EVQCNLENTSSGSPFLCNLYATALLKQSGFQFASVYQITKKNYISFPAWGLQPHL	420
361	EVQCNLENTSSGSPFLCNLYATALLKQSGFQFASVYQITKKNYISFPAWGLQPHL	420
421	LQSLQSH 428	
421	LQSLQSH 428	

RESULT 2
 US-09-608-285A-5
 1 US-09-608-285A-5 Application US/09608285A
 2 Sequence 5, 635011
 3 Patent No. 635011
 4 GENERAL INFORMATION:
 5 APPLICANT: Ford, John
 6 INVENTOR: Ford, John
 7 APPLICANT: Yeung, George
 8 INVENTOR: Yeung, George
 9 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD35-LIKE
 10 POLYPEPTIDES
 11 INTERNATIONAL CLASSIFICATION
 12 CURRENT APPLICATION NUMBER: US/09/608,285A
 13 CURRENT FILING DATE: 2000-06-30
 14 PRIOR APPLICATION NUMBER: US/09/583,231
 15 PRIOR FILING DATE: 1999-07-09
 16 PRIOR APPLICATION NUMBER: US/09/457,800
 17 PRIOR FILING DATE: 2000-04-25
 18 PRIOR APPLICATION NUMBER: 09/481,238
 19 PRIOR FILING DATE: 1999-07-09
 20 PRIOR APPLICATION NUMBER: 09/370,265
 21 PRIOR FILING DATE: 1999-08-09
 22 PRIOR APPLICATION NUMBER: PCT/US99/16180
 23 PRIOR FILING DATE: 1999-07-09
 24 PRIOR APPLICATION NUMBER: 07/350,836
 25 PRIOR FILING DATE: 1999-07-09
 26 PRIOR APPLICATION NUMBER: 07/273,447
 27 PRIOR FILING DATE: 1999-07-09
 28 PRIOR APPLICATION NUMBER: 09/244,444
 29 PRIOR FILING DATE: 1999-02-04
 30 PRIOR APPLICATION NUMBER: 09/122,449
 31 PRIOR FILING DATE: 1999-07-09
 32 PRIOR APPLICATION NUMBER: 09/118,205
 33 PRIOR FILING DATE: 1998-07-16
 34 NUMBER OF SEQ ID NOS: 60
 35 SOURCE: PatentIn Ver. 2.0
 36 SEQ ID NO 5
 37 LENGTH: 428
 38 TYPE: CDS
 39 ORGANISM: Homo sapiens
 40 US-09-608-285A-5

RESULT 3
1 SEQUENCE 6, Application US/09240639
2
3 GENERAL INFORMATION:
4 APPLICANT: Chadwick, Brian Paul
5 APPLICANT ATTORNEY: Chadwick, Brian Paul
6 INVENTOR: Chadwick, Brian Paul
7 TITLE OF INVENTION: POLYPEPTIDES AND NUCLEOTIDE SEQUENCES
8 FILE REFERENCE: 9598-066
9 PRIORITY CLAIMING DATE: US/09/240,639
10 CURRENT FILING DATE: 1998-01-28
11 CURRENT CL. NO.: 29
12 SOFTWARE: Parent In Ver. 2.0
13 LENGTH: 428
14 TYPE: PRT
15 ORGANISM: Homo sapiens
16 ORGANISM: Homo sapiens

RESULT 3

Sequence 6, Application US/09240639
US-09-240-639-6

GENERAL INFORMATION:

APPLICANT: Chaeiwick Brian Paul
APPLICANT ADDRESS: 1800 S. Bascom Ave.
Palo Alto, CA 94304-5078
TITLE OF INVENTOR: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT PILING DATE: US/09240,639
CURRENT PILING DATE NUMBER: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent Ver. 2.0
SEQ LENGTH: 428

TYPE: PRt Homo sapiens

ORGANISM: Homo sapiens

SEQUENCE:

QY 241 SYLGGLKAAKLATLGALETGDTGHTFRSACLPLKLEAKNI:FGVKYQYGGNGEYGF 300
 Db 241 SYLGGLKAAKLATLGALETGDTGHTFRSACLPLKLEAKNI:FGVKYQYGGNGEYGF 300
 QY 301 BPCYAEVLVVRGKLLHQBEVQSGVSFAFYSDYDAVDTMDIDYEGGILKVEDFERKAR 360
 Db 301 BPCYAEVLVVRGKLLHQBEVQSGVSFAFYSDYDAVDTMDIDYEGGILKVEDFERKAR 360
 QY 361 EVCNLENTFTSGSPFLCDLSYITALLKOGFADSVLTQTKVNNIETGVALGATPHL 420
 Db 361 EVCNLENTFTSGSPFLCDLSYITALLKOGFADSVLTQTKVNNIETGVALGATPHL 420
 QY 421 LOSLGISH 428
 Db 421 LOSLGISH 428

RESULT 4
 US-09-240-639-9
 ; Sequence 9: Application US/09240639
 ; GENERAL INFORMATION:
 ; APPLICANT: Chadwick, Brian Paul
 ; APPLICANT: Frischauf, Anna-Maria
 ; TITLE OF INVENTION: POLYPEPTIDES AND COMPOSITIONS RELATING TO CD39-LIKE
 ; FILE REFERENCE: 9598-066
 ; CURRENT APPLICATION NUMBER: US/09/240,639
 ; CURRENT FILING DATE: 1998-01-29
 ; PRIORITY DATE: 1999-02-24
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 428
 ; ORGANISM: Homo sapiens
 US-09-240-639-9

Query Match 100.0%; Score 2250; DB 4; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3,9e-248;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATSGTGFVFLNVCVCSAVSHRNQQTWFGEGIFSSWCPIWVSGASTYGVIFDAGSTGT 60
 Db 1 MATSGTGFVFLNVCVCSAVSHRNQQTWFGEGIFSSWCPIWVSGASTYGVIFDAGSTGT 60
 QY 61 RHVYTVQVQKQGLPILLEGVEFVSYKGLSAPVQKQAGETVQGLLEVAQDSIPRSHW 120
 Db 61 RHVYTVQVQKQGLPILLEGVEFVSYKGLSAPVQKQAGETVQGLLEVAQDSIPRSHW 120
 QY 121 KCTPVLLKATGLLPERHAKALLPEVAIEFRKSPFLPKGSVSI:MGSDGGLIANTV 180
 Db 121 KCTPVLLKATGLLPERHAKALLPEVAIEFRKSPFLPKGSVSI:MGSDGGLIANTV 180
 QY 181 NFLTQGLHGHQBTVTGLDGGASTQTITLPOETKLETPRGILTSPFNSTYLYTH 240
 Db 181 NFLTQGLHGHQBTVTGLDGGASTQTITLPOETKLETPRGILTSPFNSTYLYTH 240
 QY 241 SYLGGLKAAKLATLGALETGDTGHTFRSACLPLKLEAKNI:FGVKYQYGGNGEYGF 300
 Db 241 SYLGGLKAAKLATLGALETGDTGHTFRSACLPLKLEAKNI:FGVKYQYGGNGEYGF 300
 QY 301 BPCYAEVLVVRGKLLHQBEVQSGVSFAFYSDYDAVDTMDIDYEGGILKVEDFERKAR 360
 Db 301 BPCYAEVLVVRGKLLHQBEVQSGVSFAFYSDYDAVDTMDIDYEGGILKVEDFERKAR 360
 QY 361 EVCNLENTFTSGSPFLCDLSYITALLKOGFADSVLTQTKVNNIETGVALGATPHL 420
 Db 361 EVCNLENTFTSGSPFLCDLSYITALLKOGFADSVLTQTKVNNIETGVALGATPHL 420
 QY 421 LOSLGISH 428
 Db 421 LOSLGISH 428

RESULT 5
 US-09-350-836B-3
 ; Sequence 3: Application US/09350836B
 ; Patent No. 6387645
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
 ; FILE REFERENCE: 9598-066
 ; CURRENT APPLICATION NUMBER: US/09/350,836B
 ; CURRENT FILING DATE: 1999-07-09
 ; PRIORITY DATE: 1999-03-19
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR FILING DATE: 1999-02-24
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 428
 ; ORGANISM: Homo sapiens
 US-09-350-836B-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3,9e-248;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATSGTGFVFLNVCVCSAVSHRNQQTWFGEGIFSSWCPIWVSGASTYGVIFDAGSTGT 60
 Db 1 MATSGTGFVFLNVCVCSAVSHRNQQTWFGEGIFSSWCPIWVSGASTYGVIFDAGSTGT 60
 QY 61 RHVYTVQVQKQGLPILLEGVEFVSYKGLSAPVQKQAGETVQGLLEVAQDSIPRSHW 120
 Db 61 RHVYTVQVQKQGLPILLEGVEFVSYKGLSAPVQKQAGETVQGLLEVAQDSIPRSHW 120
 QY 121 KCTPVLLKATGLLPERHAKALLPEVAIEFRKSPFLPKGSVSI:MGSDGGLIANTV 180
 Db 121 KCTPVLLKATGLLPERHAKALLPEVAIEFRKSPFLPKGSVSI:MGSDGGLIANTV 180
 QY 181 NFLTQGLHGHQBTVTGLDGGASTQTITLPOETKLETPRGILTSPFNSTYLYTH 240
 Db 181 NFLTQGLHGHQBTVTGLDGGASTQTITLPOETKLETPRGILTSPFNSTYLYTH 240
 QY 241 SYLGGLKAAKLATLGALETGDTGHTFRSACLPLKLEAKNI:FGVKYQYGGNGEYGF 300
 Db 241 SYLGGLKAAKLATLGALETGDTGHTFRSACLPLKLEAKNI:FGVKYQYGGNGEYGF 300
 QY 301 BPCYAEVLVVRGKLLHQBEVQSGVSFAFYSDYDAVDTMDIDYEGGILKVEDFERKAR 360
 Db 301 BPCYAEVLVVRGKLLHQBEVQSGVSFAFYSDYDAVDTMDIDYEGGILKVEDFERKAR 360
 QY 361 EVCNLENTFTSGSPFLCDLSYITALLKOGFADSVLTQTKVNNIETGVALGATPHL 420
 Db 361 EVCNLENTFTSGSPFLCDLSYITALLKOGFADSVLTQTKVNNIETGVALGATPHL 420
 QY 421 LOSLGISH 428
 Db 421 LOSLGISH 428

RESULT 6
 US-09-350-836B-5
 ; Sequence 5: Application US/09350836B
 ; Patent No. 6387645
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
 ; FILE REFERENCE: 28110/35761
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: US/09/350,836
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-07-16
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 528
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-350-836b-5

 Query Match 100.0%; Score 2250; DB 4; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3, gc=248;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MATKNTVFMGVCVCANVHNOOQWTFEISGNCVINSASTVGMHQAAGSTGT 60
 Db 1 MATKNTVFMGVCVCANVHNOOQWTFEISGNCVINSASTVGMHQAAGSTGT 60

 Qy 61 RHVTVFVQMPQQLPILEGVYDSVFGSLSAFVQCPQQAETVQGLLEVAKDSI 120
 Db 61 RHVTVFVQMPQQLPILEGVYDSVFGSLSAFVQCPQQAETVQGLLEVAKDSI 120

 Qy 121 KRTVPLVATAGRLLEHKAALFVKSEIFKSPFLVPGKSVINQSDGILLAWTV 180
 Db 121 KRTVPLVATAGRLLEHKAALFVKSEIFKSPFLVPGKSVINQSDGILLAWTV 180

 Qy 181 NFVQGLHGRQETVGTLDGGASTQTFLQPEKTLTQPGTLTSEFMNSTYLKTH 240
 Db 181 NFVQGLHGRQETVGTLDGGASTQTFLQPEKTLTQPGTLTSEFMNSTYLKTH 240

 Qy 241 SYTGFLGAARLATGALTEGTGHTFRACLPMLAEIMFGVYKQNGQGEVGF 300
 Db 241 SYTGFLGAARLATGALTEGTGHTFRACLPMLAEIMFGVYKQNGQGEVGF 300

 Qy 301 EPCYAVLVKRGKLRQPEVQGFSPAFSYTYDRAVDTMDIYKGGILKVEDFERAK 360
 Db 301 EPCYAVLVKRGKLRQPEVQGFSPAFSYTYDRAVDTMDIYKGGILKVEDFERAK 360

 Qy 361 EVCNLENFTSGSPFLCNLSYITALLKQGFADSTVLTQTKNNIETGALGATHL 420
 Db 361 EVCNLENFTSGSPFLCNLSYITALLKQGFADSTVLTQTKNNIETGALGATHL 420

 Qy 421 LQSLGISH 428
 Db 421 LQSLGISH 428

RESULT 7

US-09-370-265-3
 US-09-370-265-3 Application US/09370265
 ; Patent No. 6447771
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; INVENTOR: Ford, John
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; FILE REFERENCE: 2811/35908
 ; CURRENT APPLICATION NUMBER: US/09/370,265
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; EARLIER FILING DATE: 1999-07-16
 ; EARLIER APPLICATION NUMBER: 09/350,836

; EARLIER FILING DATE: 1999-07-09
 ; EARLIER APPLICATION NUMBER: 09/273,447
 ; EARLIER FILING DATE: 1999-03-19
 ; EARLIER APPLICATION NUMBER: 09/244,444
 ; EARLIER FILING DATE: 1999-07-16
 ; EARLIER APPLICATION NUMBER: 09/122,449
 ; EARLIER FILING DATE: 1998-07-24
 ; EARLIER APPLICATION NUMBER: 09/118,205
 ; EARLIER FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-370-265-3

 Query Match 100.0%; Score 2250; DB 4; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3, gc=248;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MATKNTVFMGVCVCANVHNOOQWTFEISGNCVINSASTVGMHQAAGSTGT 60
 Db 1 MATKNTVFMGVCVCANVHNOOQWTFEISGNCVINSASTVGMHQAAGSTGT 60

 Qy 61 RHVTVFVQMPQQLPILEGVYDSVFGSLSAFVQCPQQAETVQGLLEVAKDSI 120
 Db 61 RHVTVFVQMPQQLPILEGVYDSVFGSLSAFVQCPQQAETVQGLLEVAKDSI 120

 Qy 121 KRTVPLVATAGRLLEHKAALFVKSEIFKSPFLVPGKSVINQSDGILLAWTV 180
 Db 121 KRTVPLVATAGRLLEHKAALFVKSEIFKSPFLVPGKSVINQSDGILLAWTV 180

 Qy 181 NFVQGLHGRQETVGTLDGGASTQTFLQPEKTLTQPGTLTSEFMNSTYLKTH 240
 Db 181 NFVQGLHGRQETVGTLDGGASTQTFLQPEKTLTQPGTLTSEFMNSTYLKTH 240

 Qy 241 SYTGFLGAARLATGALTEGTGHTFRACLPMLAEIMFGVYKQNGQGEVGF 300
 Db 241 SYTGFLGAARLATGALTEGTGHTFRACLPMLAEIMFGVYKQNGQGEVGF 300

 Qy 301 EPCYAVLVKRGKLRQPEVQGFSPAFSYTYDRAVDTMDIYKGGILKVEDFERAK 360
 Db 301 EPCYAVLVKRGKLRQPEVQGFSPAFSYTYDRAVDTMDIYKGGILKVEDFERAK 360

 Qy 361 EVCNLENFTSGSPFLCNLSYITALLKQGFADSTVLTQTKNNIETGALGATHL 420
 Db 361 EVCNLENFTSGSPFLCNLSYITALLKQGFADSTVLTQTKNNIETGALGATHL 420

 Qy 421 LQSLGISH 428
 Db 421 LQSLGISH 428

RESULT 8

US-09-370-265-5
 US-09-370-265-5 Application US/09370265
 ; Patent No. 6447771
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; INVENTOR: Ford, John
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; FILE REFERENCE: 2811/35908
 ; CURRENT APPLICATION NUMBER: US/09/370,265
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; EARLIER FILING DATE: 1999-08-09
 ; EARLIER FILING DATE: 1999-07-16
 ; EARLIER APPLICATION NUMBER: 09/350,836
 ; EARLIER FILING DATE: 1999-07-09
 ; EARLIER APPLICATION NUMBER: 09/273,444
 ; EARLIER FILING DATE: 1999-03-19
 ; EARLIER APPLICATION NUMBER: 09/244,444

/ EARLIER FILING DATE: 1999-02-04
 / EARLIER APPLICATION NUMBER: 09/122,449
 / EARLIER FILING DATE: 1998-07-24
 / EARLIER FILING DATE: 1998-07-24
 / EARLIER FILING DATE: 1998-07-16
 / NUMBER OF SEQ ID NOS: 37
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 1: 428
 / LENGTH: 428
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-370-265-5

Query Match 100.0%; Score 2250; DB 4; Length 428;

Best Local Similarity 100.0%; Pred. No. 3,96-248; Indels 0; Gaps 0;
Matches 428; Conservative 0; Mismatches 0;

QY 1 WATSGTGVFFMLVSWCVSAVSHNNQOTWFGIFLSSMCPINVASITLYGIMFDAGSTGT 60
 DB 1 WATSGTGVFFMLVSWCVSAVSHNNQOTWFGIFLSSMCPINVASITLYGIMFDAGSTGT 60
 QY 61 RHIVYTVQVMHQGPOLPILEGVDFVSGKLSAFVDPQKGAETVOGLLEVAKDSIPRSH 120
 DB 61 RHIVYTVQVMHQGPOLPILEGVDFVSGKLSAFVDPQKGAETVOGLLEVAKDSIPRSH 120
 QY 121 KKTGVLTAKAGLLPHEKAKALLFVKETFKSPFLVPKGSVSMGSDGILAWTV 180
 DB 121 KKTGVLTAKAGLLPHEKAKALLFVKETFKSPFLVPKGSVSMGSDGILAWTV 180
 QY 181 NFLTQVQHGHRQETVGLDGGASTQITFLPOEKTLEOTPRGLVTSFEMFNSTYKLYTH 240
 DB 181 NFLTQVQHGHRQETVGLDGGASTQITFLPOEKTLEOTPRGLVTSFEMFNSTYKLYTH 240
 QY 241 SYLGGLVKAARLALGALTEGTDGHTFSACLPMLLEAKNIFGGVYKVGNGEVEGF 300
 DB 241 SYLGGLVKAARLALGALTEGTDGHTFSACLPMLLEAKNIFGGVYKVGNGEVEGF 300
 QY 301 BPCVAVLVVRGKLHQPEEVQSGSVYASVYVDAVDTMDVDEKGLLYEDFERKAR 360
 DB 301 BPCVAVLVVRGKLHQPEEVQSGSVYASVYVDAVDTMDVDEKGLLYEDFERKAR 360
 QY 361 EVCMDLENTSGSFFLMDLSTALLKGGFPAQSTVLQTKVNNLETGVALGATFLH 420
 DB 361 EVCMDLENTSGSFFLMDLSTALLKGGFPAQSTVLQTKVNNLETGVALGATFLH 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 6
 US-09-557-800C-3
 / Sequence 3, Application US/09557800C
 / Patent No. 6476211
 / GENERAL INFORMATION:
 / APPLICANT: Mulero, John
 / APPLICANT: Mulero, Julio
 / APPLICANT: Young, George
 / TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
 / FILE REFERENCE: 28110/3645
 / CURRENT APPLICATION NUMBER: US/09/557,800C
 / CURRENT FILING DATE: 2000-04-25
 / PRIOR FILING DATE: 2000-04-25
 / PRIOR FILING DATE: 2000-04-25
 / PRIOR FILING DATE: 1999-08-09
 / PRIOR FILING DATE: 1999-08-09
 / PRIOR FILING DATE: 1999-08-09
 / PRIOR FILING DATE: 1999-07-09
 / PRIOR FILING DATE: 1999-03-19

/ PRIOR APPLICATION NUMBER: 09/122,449
 / PRIOR FILING DATE: 1998-07-24
 / PRIOR APPLICATION NUMBER: 09/244,444
 / PRIOR FILING DATE: 1998-07-24
 / PRIOR APPLICATION NUMBER: 09/118,205
 / PRIOR FILING DATE: 1998-07-16
 / NUMBER OF SEQ ID NOS: 56
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 3: 428
 / LENGTH: 428
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-557-800C-3

Query Match 100.0%; Score 2250; DB 4; Length 428;

Best Local Similarity 100.0%; Pred. No. 3,96-248; Indels 0; Gaps 0;
Matches 428; Conservative 0; Mismatches 0;

QY 1 WATSGTGVFFMLVSWCVSAVSHNNQOTWFGIFLSSMCPINVASITLYGIMFDAGSTGT 60
 DB 1 WATSGTGVFFMLVSWCVSAVSHNNQOTWFGIFLSSMCPINVASITLYGIMFDAGSTGT 60
 QY 61 RHIVYTVQVMHQGPOLPILEGVDFVSGKLSAFVDPQKGAETVOGLLEVAKDSIPRSH 120
 DB 61 RHIVYTVQVMHQGPOLPILEGVDFVSGKLSAFVDPQKGAETVOGLLEVAKDSIPRSH 120
 QY 121 KKTGVLTAKAGLLPHEKAKALLFVKETFKSPFLVPKGSVSMGSDGILAWTV 180
 DB 121 KKTGVLTAKAGLLPHEKAKALLFVKETFKSPFLVPKGSVSMGSDGILAWTV 180
 QY 181 NFLTQVQHGHRQETVGLDGGASTQITFLPOEKTLEOTPRGLVTSFEMFNSTYKLYTH 240
 DB 181 NFLTQVQHGHRQETVGLDGGASTQITFLPOEKTLEOTPRGLVTSFEMFNSTYKLYTH 240
 QY 241 SYLGGLVKAARLALGALTEGTDGHTFSACLPMLLEAKNIFGGVYKVGNGEVEGF 300
 DB 241 SYLGGLVKAARLALGALTEGTDGHTFSACLPMLLEAKNIFGGVYKVGNGEVEGF 300
 QY 301 BPCVAVLVVRGKLHQPEEVQSGSVYASVYVDAVDTMDVDEKGLLYEDFERKAR 360
 DB 301 BPCVAVLVVRGKLHQPEEVQSGSVYASVYVDAVDTMDVDEKGLLYEDFERKAR 360
 QY 361 EVCMDLENTSGSFFLMDLSTALLKGGFPAQSTVLQTKVNNLETGVALGATFLH 420
 DB 361 EVCMDLENTSGSFFLMDLSTALLKGGFPAQSTVLQTKVNNLETGVALGATFLH 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 10
 US-09-557-800C-5
 / Sequence 5, Application US/09557800C
 / Patent No. 6476211
 / GENERAL INFORMATION:
 / APPLICANT: Mulero, John
 / APPLICANT: Mulero, Julio
 / APPLICANT: Young, George
 / TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
 / FILE REFERENCE: 28110/3645
 / CURRENT APPLICATION NUMBER: US/09/557,800C
 / CURRENT FILING DATE: 2000-04-25
 / PRIOR FILING DATE: 2000-04-25
 / PRIOR FILING DATE: 2000-04-25
 / PRIOR FILING DATE: 1999-08-09
 / PRIOR FILING DATE: 1999-08-09
 / PRIOR FILING DATE: 1999-08-09
 / PRIOR FILING DATE: 1999-07-09
 / PRIOR FILING DATE: 1999-03-19

; PRIOR FILING DATE: 1999-09-19
 ; PRIOR APPLICATION NUMBER: 09/122449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244444
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR APPLICATION NUMBER: 09/118 205
 ; NUMBER OF SEQ ID NOS: 56
 ; SEQ ID NO 5 PatentIn Ver. 2.0
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-357-800C-5

Query Match 100.0%; Score 2250; DB 4; Length 428;

Best Local Similarity 100.0%; Pred. No. 3.9e+248;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATSNGTVFVFLMVCSCVSAVSHRNQOTWFEGLFLSKMCPINVSASTLYGIMFADSGTGT 60
 Db 1 MATSNGTVFVFLMVCSCVSAVSHRNQOTWFEGLFLSKMCPINVSASTLYGIMFADSGTGT 60
 Qy 61 RHVHTVFVQVQPCQPLLEGEVFSVKGSLSAFVDQPKQAGETVOGLLEKAVKDSIPRSH 120
 Db 61 RHVHTVFVQVQPCQPLLEGEVFSVKGSLSAFVDQPKQAGETVOGLLEKAVKDSIPRSH 120
 Qy 121 KXTPVVLTATAGLLPEHKAALLFEVKEIFRKSFPFLVPGKSVIMQSGDGLIAWTV 180
 Db 121 KXTPVVLTATAGLLPEHKAALLFEVKEIFRKSFPFLVPGKSVIMQSGDGLIAWTV 180
 Qy 181 NLTGQVGHQHQETVGTLDLGGASTQITLPOFEKTELEOTPRGYTSPFMSNTYKLTH 240
 Db 181 NLTGQVGHQHQETVGTLDLGGASTQITLPOFEKTELEOTPRGYTSPFMSNTYKLTH 240
 Qy 241 SYLGFLCAKARLATLGALETGTOGHTFRSACLPRMLEARMIEGQVYKYGNOGEVGF 300
 Db 241 SYLGFLCAKARLATLGALETGTOGHTFRSACLPRMLEARMIEGQVYKYGNOGEVGF 300
 Qy 301 EFCYAEVLVRVKLHQPEVQKSGSVAFSVYDRAVDQIMDIYKGGILKVEDFERAK 360
 Db 301 EFCYAEVLVRVKLHQPEVQKSGSVAFSVYDRAVDQIMDIYKGGILKVEDFERAK 360
 Qy 361 EVCNMLENTFGSPFLCNDLSYTTALLHCGFGRASSTVQLTKNNIETGVALGATHL 420
 Db 361 EVCNMLENTFGSPFLCNDLSYTTALLHCGFGRASSTVQLTKNNIETGVALGATHL 420
 Qy 421 LQSLGISH 428
 Db 421 LQSLGISH 428

RESULT 11
 US-09-608-285A-7

; Sequence 7, Application US/09608285A
 ; Patent No. 635013
 ; Applicant: Genentech, Inc.
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Yeung, George
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; FILE REFERENCE: 28110/36570
 ; CURRENT APPLICATION NUMBER: US/09/608,285A
 ; PRIOR APPLICATION NUMBER: US/09/063,231
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 09/557,800
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/461,238
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 1999-08-09

; PRIOR APPLICATION NUMBER: ECT/US99/16180
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; NUMBER OF SEQ ID NOS: 60
 ; SEQ ID NO 7 PatentIn Ver. 2.0
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-608-205A-7

Query Match 99.3%; Score 2235; DB 4; Length 428;

Best Local Similarity 99.3%; Pred. No. 2e+246;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MATSNGTVFVFLMVCSCVSAVSHRNQOTWFEGLFLSKMCPINVSASTLYGIMFADSGTGT 60
 Db 1 MATSNGTVFVFLMVCSCVSAVSHRNQOTWFEGLFLSKMCPINVSASTLYGIMFADSGTGT 60
 Qy 61 RHVHTVFVQVQPCQPLLEGEVFSVKGSLSAFVDQPKQAGETVOGLLEKAVKDSIPRSH 120
 Db 61 RHVHTVFVQVQPCQPLLEGEVFSVKGSLSAFVDQPKQAGETVOGLLEKAVKDSIPRSH 120
 Qy 121 KXTPVVLTATAGLLPEHKAALLFEVKEIFRKSFPFLVPGKSVIMQSGDGLIAWTV 180
 Db 121 KXTPVVLTATAGLLPEHKAALLFEVKEIFRKSFPFLVPGKSVIMQSGDGLIAWTV 180
 Qy 181 NLTGQVGHQHQETVGTLDLGGASTQITLPOFEKTELEOTPRGYTSPFMSNTYKLTH 240
 Db 181 NLTGQVGHQHQETVGTLDLGGASTQITLPOFEKTELEOTPRGYTSPFMSNTYKLTH 240
 Qy 241 SYLGFLCAKARLATLGALETGTOGHTFRSACLPRMLEARMIEGQVYKYGNOGEVGF 300
 Db 241 SYLGFLCAKARLATLGALETGTOGHTFRSACLPRMLEARMIEGQVYKYGNOGEVGF 300
 Qy 301 EFCYAEVLVRVKLHQPEVQKSGSVAFSVYDRAVDQIMDIYKGGILKVEDFERAK 360
 Db 301 EFCYAEVLVRVKLHQPEVQKSGSVAFSVYDRAVDQIMDIYKGGILKVEDFERAK 360
 Qy 361 EVCNMLENTFGSPFLCNDLSYTTALLHCGFGRASSTVQLTKNNIETGVALGATHL 420
 Db 361 EVCNMLENTFGSPFLCNDLSYTTALLHCGFGRASSTVQLTKNNIETGVALGATHL 420
 Qy 421 LQSLGISH 428
 Db 421 LQSLGISH 428

RESULT 12
 US-09-350-836B-7

; Sequence 7, Application US/09350836B
 ; Patent No. 6387645
 ; Applicant: Genentech, Inc.
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD38-LIKE
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; CURRENT APPLICATION NUMBER: US/09/350,836B
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16

```

: PRIOR APPLICATION NUMBER: 09/122,449
:
: PRIOR FILING DATE: 1998-07-24
: PRIOR APPLICATION NUMBER: 09/244,444
: PRIOR FILING DATE: 1999-02-04
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 7
: LENGTH: 428
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-350-836B-7

```

Query Match	99.3%: Score 2235; DB 4; Length 428;
Best Local Similarity	99.3%: Pred. No. 2e-246;
Matches	425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 MATSNGTIFGVCVCVCAVSHRNQWTFESIFLSSNCGIVASATVXCTMFADAGSTGT 60
Db	1 MATSNGTIFGVCVCVCAVSHRNQWTFESIFLSSNCGIVASATVXCTMFADAGSTGT 60
Qy	61 RHNYTTFVQNSGQIFLPEHPSRVCAGKSLFVQSKQCHTQVQGLVENSQSTFASH 120
Db	61 RHNYTTFVQNSGQIFLPEHPSRVCAGKSLFVQSKQCHTQVQGLVENSQSTFASH 120
Qy	61 RHNYTTFVQNSGQIFLPEHPSRVCAGKSLFVQSKQCHTQVQGLVENSQSTFASH 120
Db	61 RHNYTTFVQNSGQIFLPEHPSRVCAGKSLFVQSKQCHTQVQGLVENSQSTFASH 120
Qy	121 KATVVLATAGLAPLLPEHAKVALLPEVKELFKPSFPFVPGNSVINTQDDEGLFANVT 180
Db	121 KATVVLATAGLAPLLPEHAKVALLPEVKELFKPSFPFVPGNSVINTQDDEGLFANVT 180
Qy	121 KATVVLATAGLAPLLPEHAKVALLPEVKELFKPSFPFVPGNSVINTQDDEGLFANVT 180
Db	121 KATVVLATAGLAPLLPEHAKVALLPEVKELFKPSFPFVPGNSVINTQDDEGLFANVT 180
Qy	181 NFIQTGLQHGRTGTGLDAGASSTQITPEKTELTGTATGTLSTFEMNFTSKLYTH 240
Db	181 NFIQTGLQHGRTGTGLDAGASSTQITPEKTELTGTATGTLSTFEMNFTSKLYTH 240
Qy	181 NFIQTGLQHGRTGTGLDAGASSTQITPEKTELTGTATGTLSTFEMNFTSKLYTH 240
Db	181 NFIQTGLQHGRTGTGLDAGASSTQITPEKTELTGTATGTLSTFEMNFTSKLYTH 240
Qy	241 SYLGFGLAARLALGALTEGTGTFRSACFMELAEVIFGVKQVGGQSGEWF 300
Db	241 SYLGFGLAARLALGALTEGTGTFRSACFMELAEVIFGVKQVGGQSGEWF 300
Qy	241 SYLGFGLAARLALGALTEGTGTFRSACFMELAEVIFGVKQVGGQSGEWF 300
Db	241 SYLGFGLAARLALGALTEGTGTFRSACFMELAEVIFGVKQVGGQSGEWF 300
Qy	301 EFCVAVLRVAKRLHDEVTGSGSVAFVYDGVADTMDVKEGGLIKVYDFEKAR 360
Db	301 EFCVAVLRVAKRLHDEVTGSGSVAFVYDGVADTMDVKEGGLIKVYDFEKAR 360
Qy	301 EFCVAVLRVAKRLHDEVTGSGSVAFVYDGVADTMDVKEGGLIKVYDFEKAR 360
Db	301 EFCVAVLRVAKRLHDEVTGSGSVAFVYDGVADTMDVKEGGLIKVYDFEKAR 360
Qy	361 EVCNLENFTSGSPFLCMLSYLTALLKQDFQFADSTVGLQTEKVNLETCFVALGNTHL 420
Db	361 EVCNLENFTSGSPFLCMLSYLTALLKQDFQFADSTVGLQTEKVNLETCFVALGNTHL 420
Qy	361 EVCNLENFTSGSPFLCMLSYLTALLKQDFQFADSTVGLQTEKVNLETCFVALGNTHL 420
Db	361 EVCNLENFTSGSPFLCMLSYLTALLKQDFQFADSTVGLQTEKVNLETCFVALGNTHL 420
Qy	421 LQSLQISH 128
Db	421 LQSLQISH 128

RESULT 13

US-09-370-265-7
Sequence 7, Application US/09370265
Patent No. 6447771
GENETIC FORECLOSURE
APPLICANT: NATURE JOHN
APPLICANT: MATEO JULIO
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
FILE REFERENCE: 2811/35908 US/09/370_265
PRIORITY DATE: 09/03/08
CURRENT FILING DATE: 1998-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 09/350,436
EARLIER FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 09/327,447
EARLIER FILING DATE: 1998-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16

[illegible]

RESULT 14
 US-09-557-800C-7
 Sequence 7, Application US/09557800C
 Title: Polypeptides
 GENERAL INFORMATION:
 APPLICANT: Ford, John
 APPLICANT: Mulero, Julio
 APPLICANT: Wang, George
 TITLE INVENTOR: Polypeptides
 TITLE INVENTION: Polypeptides
 FILE REFERENCE: US/09/557,800C
 CURRENT APPLICATION NUMBER: 28110/36457
 PRIORITY APPLICATION NUMBER: 09/481,238
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: 09/370,265
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 09/370,265
 PRIOR FILING DATE: 1998-07-16
 PRIOR APPLICATION NUMBER: 09/350836
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: 09/373447
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 09/122449
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 09/244444
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 09/118,205

```

; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: prt
; ORGANISM: Homo sapiens

```

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%;
Pred. No. 2e-246;
Matches 425; Conservative 0; Mismatches 3; Indels

[illegible]

RESULT 15
Sequence 25 Application US/09608285A
US-09-608-285A-25

GENERAL INFORMATION:
APPLICANT: Ford, John
INVENTOR: Ford, George
TITLE OF INVENTION: POLYETHYLENES
POLYETHYLENES
CURRENT FILING DATE: US/09/608285A
CURRENT APPLICATION NUMBER: 09-608-25
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,233
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/581,481
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/370,262
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 09/350,830
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/350,830
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/373,441
PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 05/244,444
 ; PRIOR FILING DATE: 1992-02-04
 ; PRIOR APPLICATION NUMBER: 05/122,449
 ; PRIOR FILING DATE: 1992-02-04
 ; PRIOR APPLICATION NUMBER: 05/118,205
 ; PRIOR FILING DATE: 1992-07-16
 ; NUMBER OF SEQ ID NOS: 60
 ; COMPLETE SEQUENCE LISTING IN SEQ ID NOS
 ; SEQ ID NO 25
 ; LENGTH: 405
 ; TYPE: 5'UT Homo sapiens
 ; ORGANISM: Homo sapiens
 ; US-03-008-2856-25

Query Match	93.5%	Score 2104	Dr. 41	Length 405
Best Local Similarity	100.0%	Pred. No. 176-231		
Matches	400	Conservative	0	Mismatches 0
			Indels	Gaps 0
1	MATSGTGVFVMLVVCVCSVAISHNRQVQFEGFLSSMCDDINVGASTVIGIMEDAGSTG	60		
Q				
1	MATSGTGVFVMLVVCVCSVAISHNRQVQFEGFLSSMCDDINVGASTVIGIMEDAGSTG	60		
D				
61	RHHVTVVQVHKQCPQLLEEVEFVSVPKGLSAFVQKQAGETVQGLLEWAKQDSIPSHS	120		
Q				
1	RHHVTVVQVHKQCPQLLEEVEFVSVPKGLSAFVQKQAGETVQGLLEWAKQDSIPSHS	120		
D				
121	KTYVYKATGALGRLPEHKAALFEVBEIKPSKSPFLVPKGSVYVQSSDEGLVAMVTV	180		
Q				
121	KTYVYKATGALGRLPEHKAALFEVBEIKPSKSPFLVPKGSVYVQSSDEGLVAMVTV	180		
D				
131	KTYVYKATGALGRLPEHKAALFEVBEIKPSKSPFLVPKGSVYVQSSDEGLVAMVTV	180		
Q				
181	NFLPGVGHGHRQVETGTDLGGASGTQIFLPQEKTLQTPRGVLTSPFEMFNSTKVLVTH	240		
Q				
181	NFLPGVGHGHRQVETGTDLGGASGTQIFLPQEKTLQTPRGVLTSPFEMFNSTKVLVTH	240		
D				
241	SVYLGFGKAAEALGATLEGTDTGHTFSPACLPFLMEWIFPGGVYVQVGGNQEVEVF	300		
Q				
241	SVYLGFGKAAEALGATLEGTDTGHTFSPACLPFLMEWIFPGGVYVQVGGNQEVEVF	300		
D				
301	EFCVAVLVAVRCKHQPVEVQGVGSYASVYDVAQNTDMQVGGKGLVYEDFERKAR	360		
Q				
301	EFCVAVLVAVRCKHQPVEVQGVGSYASVYDVAQNTDMQVGGKGLVYEDFERKAR	360		
D				
341	EFCVAVLVAVRCKHQPVEVQGVGSYASVYDVAQNTDMQVGGKGLVYEDFERKAR	400		
Q				
341	EFCVAVLVAVRCKHQPVEVQGVGSYASVYDVAQNTDMQVGGKGLVYEDFERKAR	400		
D				
361	EFCVAVLVAVRCKHQPVEVQGVGSYASVYDVAQNTDMQVGGKGLVYEDFERKAR	400		
D				

Search completed: November 13, 2003, 06:24:36
Job time : 22 secs

FT	CARBHYD	42	42	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBHYD	232	232	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBHYD	368	368	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	SEQUENCE	428 AA	47517 MW	393432AL350540D0 C6047	
Query Match		100.0%	Score 2250	DB 1	Length 428
Best Local Similarity		100.0%	Prod. No. 3.3e-1473		
Matches 428		Conservative 0	Kimatches 0	Indels 0	Gaps 0
QY	QY	1	MATSGTGVFVFLVVCVCSVNSRHQNTWFGIISFKPCVFNVSASTLVGIWFGAGTGT	60	
DQ	DQ	1	MATSGTGVFVFLVVCVCSVNSRHQNTWFGIISFKPCVFNVSASTLVGIWFGAGTGT	60	
DQ	DQ	61	RHIVTFTVQWQFQPLTLEGVSDVSKVSLAFVQPKQZATVQGLLEVAQDPSRHW	120	
DQ	DQ	61	RHIVTFTVQWQFQPLTLEGVSDVSKVSLAFVQPKQZATVQGLLEVAQDPSRHW	120	
QY	QY	121	KCTPVLTATGATGALLPEKVKALKVLEIKFKSPFLPVLPGVSNIMQSGDGLAVTNY	180	
DQ	DQ	121	KCTPVLTATGATGALLPEKVKALKVLEIKFKSPFLPVLPGVSNIMQSGDGLAVTNY	180	
QY	QY	181	NFLTGQAGHRETVGTLDDAGAGTQITLPAFENLEQTQGLTSLTGLVTH	240	
QY	QY	241	SYGFLHAAKATLQALSTFQDQNTFSSACPLWLEHVIQGTQATGQNGQGVGF	300	
DQ	DQ	241	SYGFLHAAKATLQALSTFQDQNTFSSACPLWLEHVIQGTQATGQNGQGVGF	300	
QY	QY	301	ECVATVLRVVRGKHQDPEVQSGVFARVYDVAVDVNDIVKEGGLIKVDEPKAR	360	
DQ	DQ	301	ECVATVLRVVRGKHQDPEVQSGVFARVYDVAVDVNDIVKEGGLIKVDEPKAR	360	
QY	QY	361	EVCNDLNFSTGSPFLCNDLSYLTALDKGCFASDVTVDIMTKKGLVETGVALGATFL	420	
DQ	DQ	361	EVCNDLNFSTGSPFLCNDLSYLTALDKGCFASDVTVDIMTKKGLVETGVALGATFL	420	
QY	QY	421	LQSGTISH 428		
DQ	DQ	421	LQSGTISH 428		

[illegible]

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the open access database. There are no restrictions on its
 CC use by non-profit institutions, as long as the database is
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: A277748; CAC16598.1;
 DR InterPro: IPR000407; GDA1_C039_NTPase.
 DR Pfam: PF01150; GDA1_C039_1; NTPase; FALSE NEG.
 DR SCOP: 33333; RNA_C039; CD39; Nucleoside triphosphatase; Magnesium;
 KN Hydrolyase; 71; 72; 73; 74; 75; 76; 77; 78; 79; 80; 81; 82; 83; 84; 85; 86; 87; 88; 89; 90; 91; 92; 93; 94; 95; 96; 97; 98; 99; 100; 101; 102; 103; 104; 105; 106; 107; 108; 109; 110; 111; 112; 113; 114; 115; 116; 117; 118; 119; 120; 121; 122; 123; 124; 125; 126; 127; 128; 129; 130; 131; 132; 133; 134; 135; 136; 137; 138; 139; 140; 141; 142; 143; 144; 145; 146; 147; 148; 149; 150; 151; 152; 153; 154; 155; 156; 157; 158; 159; 160; 161; 162; 163; 164; 165; 166; 167; 168; 169; 170; 171; 172; 173; 174; 175; 176; 177; 178; 179; 180; 181; 182; 183; 184; 185; 186; 187; 188; 189; 190; 191; 192; 193; 194; 195; 196; 197; 198; 199; 200; 201; 202; 203; 204; 205; 206; 207; 208; 209; 210; 211; 212; 213; 214; 215; 216; 217; 218; 219; 220; 221; 222; 223; 224; 225; 226; 227; 228; 229; 230; 231; 232; 233; 234; 235; 236; 237; 238; 239; 240; 241; 242; 243; 244; 245; 246; 247; 248; 249; 250; 251; 252; 253; 254; 255; 256; 257; 258; 259; 260; 261; 262; 263; 264; 265; 266; 267; 268; 269; 270; 271; 272; 273; 274; 275; 276; 277; 278; 279; 280; 281; 282; 283; 284; 285; 286; 287; 288; 289; 290; 291; 292; 293; 294; 295; 296; 297; 298; 299; 300; 301; 302; 303; 304; 305; 306; 307; 308; 309; 310; 311; 312; 313; 314; 315; 316; 317; 318; 319; 320; 321; 322; 323; 324; 325; 326; 327; 328; 329; 330; 331; 332; 333; 334; 335; 336; 337; 338; 339; 340; 341; 342; 343; 344; 345; 346; 347; 348; 349; 350; 351; 352; 353; 354; 355; 356; 357; 358; 359; 360; 361; 362; 363; 364; 365; 366; 367; 368; 369; 370; 371; 372; 373; 374; 375; 376; 377; 378; 379; 380; 381; 382; 383; 384; 385; 386; 387; 388; 389; 390; 391; 392; 393; 394; 395; 396; 397; 398; 399; 400; 401; 402; 403; 404; 405; 406; 407; 408; 409; 410; 411; 412; 413; 414; 415; 416; 417; 418; 419; 420; 421; 422; 423; 424; 425; 426; 427; 428; 429; 430; 431; 432; 433; 434; 435; 436; 437; 438; 439; 440; 441; 442; 443; 444; 445; 446; 447; 448; 449; 450; 451; 452; 453; 454; 455; 456; 457; 458; 459; 460; 461; 462; 463; 464; 465; 466; 467; 468; 469; 470; 471; 472; 473; 474; 475; 476; 477; 478; 479; 480; 481; 482; 483; 484; 485; 486; 487; 488; 489; 490; 491; 492; 493; 494; 495; 496; 497; 498; 499; 500; 501; 502; 503; 504; 505; 506; 507; 508; 509; 510; 511; 512; 513; 514; 515; 516; 517; 518; 519; 520; 521; 522; 523; 524; 525; 526; 527; 528; 529; 530; 531; 532; 533; 534; 535; 536; 537; 538; 539; 540; 541; 542; 543; 544; 545; 546; 547; 548; 549; 550; 551; 552; 553; 554; 555; 556; 557; 558; 559; 560; 561; 562; 563; 564; 565; 566; 567; 568; 569; 570; 571; 572; 573; 574; 575; 576; 577; 578; 579; 580; 581; 582; 583; 584; 585; 586; 587; 588; 589; 590; 591; 592; 593; 594; 595; 596; 597; 598; 599; 600; 601; 602; 603; 604; 605; 606; 607; 608; 609; 610; 611; 612; 613; 614; 615; 616; 617; 618; 619; 620; 621; 622; 623; 624; 625; 626; 627; 628; 629; 630; 631; 632; 633; 634; 635; 636; 637; 638; 639; 640; 641; 642; 643; 644; 645; 646; 647; 648; 649; 650; 651; 652; 653; 654; 655; 656; 657; 658; 659; 660; 661; 662; 663; 664; 665; 666; 667; 668; 669; 670; 671; 672; 673; 674; 675; 676; 677; 678; 679; 680; 681; 682; 683; 684; 685; 686; 687; 688; 689; 690; 691; 692; 693; 694; 695; 696; 697; 698; 699; 700; 701; 702; 703; 704; 705; 706; 707; 708; 709; 710; 711; 712; 713; 714; 715; 716; 717; 718; 719; 720; 721; 722; 723; 724; 725; 726; 727; 728; 729; 730; 731; 732; 733; 734; 735; 736; 737; 738; 739; 740; 741; 742; 743; 744; 745; 746; 747; 748; 749; 750; 751; 752; 753; 754; 755; 756; 757; 758; 759; 760; 761; 762; 763; 764; 765; 766; 767; 768; 769; 770; 771; 772; 773; 774; 775; 776; 777; 778; 779; 780; 781; 782; 783; 784; 785; 786; 787; 788; 789; 790; 791; 792; 793; 794; 795; 796; 797; 798; 799; 800; 801; 802; 803; 804; 805; 806; 807; 808; 809; 810; 811; 812; 813; 814; 815; 816; 817; 818; 819; 820; 821; 822; 823; 824; 825; 826; 827; 828; 829; 830; 831; 832; 833; 834; 835; 836; 837; 838; 839; 840; 841; 842; 843; 844; 845; 846; 847; 848; 849; 850; 851; 852; 853; 854; 855; 856; 857; 858; 859; 860; 861; 862; 863; 864; 865; 866; 867; 868; 869; 870; 871; 872; 873; 874; 875; 876; 877; 878; 879; 880; 881; 882; 883; 884; 885; 886; 887; 888; 889; 890; 891; 892; 893; 894; 895; 896; 897; 898; 899; 900; 901; 902; 903; 904; 905; 906; 907; 908; 909; 910; 911; 912; 913; 914; 915; 916; 917; 918; 919; 920; 921; 922; 923; 924; 925; 926; 927; 928; 929; 930; 931; 932; 933; 934; 935; 936; 937; 938; 939; 940; 941; 942; 943; 944; 945; 946; 947; 948; 949; 950; 951; 952; 953; 954; 955; 956; 957; 958; 959; 960; 961; 962; 963; 964; 965; 966; 967; 968; 969; 970; 971; 972; 973; 974; 975; 976; 977; 978; 979; 980; 981; 982; 983; 984; 985; 986; 987; 988; 989; 990; 991; 992; 993; 994; 995; 996; 997; 998; 999; 1000; 1001; 1002; 1003; 1004; 1005; 1006; 1007; 1008; 1009; 1010; 1011; 1012; 1013; 1014; 1015; 1016; 1017; 1018; 1019; 1020; 1021; 1022; 1023; 1024; 1025; 1026; 1027; 1028; 1029; 1030; 1031; 1032; 1033; 1034; 1035; 1036; 1037; 1038; 1039; 1040; 1041; 1042; 1043; 1044; 1045; 1046; 1047; 1048; 1049; 1050; 1051; 1052; 1053; 1054; 1055; 1056; 1057; 1058; 1059; 1060; 1061; 1062; 1063; 1064; 1065; 1066; 1067; 1068; 1069; 1070; 1071; 1072; 1073; 1074; 1075; 1076; 1077; 1078; 1079; 1080; 1081; 1082; 1083; 1084; 1085; 1086; 1087; 1088; 1089; 1090; 1091; 1092; 1093; 1094; 1095; 1096; 1097; 1098; 1099; 1100; 1101; 1102; 1103; 1104; 1105; 1106; 1107; 1108; 1109; 1110; 1111; 1112; 1113; 1114; 1115; 1116; 1117; 1118; 1119; 1120; 1121; 1122; 1123; 1124; 1125; 1126; 1127; 1128; 1129; 1130; 1131; 1132; 1133; 1134; 1135; 1136; 1137; 1138; 1139; 1140; 1141; 1142; 1143; 1144; 1145; 1146; 1147; 1148; 1149; 1150; 1151; 1152; 1153; 1154; 1155; 1156; 1157; 1158; 1159; 1160; 1161; 1162; 1163; 1164; 1165; 1166; 1167; 1168; 1169; 1170; 1171; 1172; 1173; 1174; 1175; 1176; 1177; 1178; 1179; 1180; 1181; 1182; 1183; 1184; 1185; 1186; 1187; 1188; 1189; 1190; 1191; 1192; 1193; 1194; 1195; 1196; 1197; 1198; 1199; 1200; 1201; 1202; 1203; 1204; 1205; 1206; 1207; 1208; 1209; 1210; 1211; 1212; 1213; 1214; 1215; 1216; 1217; 1218; 1219; 1220; 1221; 1222; 1223; 1224; 1225; 1226; 1227; 1228; 1229; 1230; 1231; 1232; 1233; 1234; 1235; 1236; 1237; 1238; 1239; 1240; 1241; 1242; 1243; 1244; 1245; 1246; 1247; 1248; 1249; 1250; 1251; 1252; 1253; 1254; 1255; 1256; 1257; 1258; 1259; 1260; 1261; 1262; 1263; 1264; 1265; 1266; 1267; 1268; 1269; 1270; 1271; 1272; 1273; 1274; 1275; 1276; 1277; 1278; 1279; 1280; 1281; 1282; 1283; 1284; 1285; 1286; 1287; 1288; 1289; 1290; 1291; 1292; 1293; 1294; 1295; 1296; 1297; 1298; 1299; 1300; 1301; 1302; 1303; 1304; 1305; 1306; 1307; 1308; 1309; 1310; 1311; 1312; 1313; 1314; 1315; 1316; 1317; 1318; 1319; 1320; 1321; 1322; 1323; 1324; 1325; 1326; 1327; 1328; 1329; 1330; 1331; 1332; 1333; 1334; 1335; 1336; 1337; 1338; 1339; 1340; 1341; 1342; 1343; 1344; 1345; 1346; 1347; 1348; 1349; 1350; 1351; 1352; 1353; 1354; 1355; 1356; 1357; 1358; 1359; 1360; 1361; 1362; 1363; 1364; 1365; 1366; 1367; 1368; 1369; 1370; 1371; 1372; 1373; 1374; 1375; 1376; 1377; 1378; 1379; 1380; 1381; 1382; 1383; 1384; 1385; 1386; 1387; 1388; 1389; 1390; 1391; 1392; 1393; 1394; 1395; 1396; 1397; 1398; 1399; 1400; 1401; 1402; 1403; 1404; 1405; 1406; 1407; 1408; 1409; 1410; 1411; 1412; 1413; 1414; 1415; 1416; 1417; 1418; 1419; 1420; 1421; 1422; 1423; 1424; 1425; 1426; 1427; 1428; 1429; 1430; 1431; 1432; 1433; 1434; 1435; 1436; 1437; 1438; 1439; 1440; 1441; 1442; 1443; 1444; 1445; 1446; 1447; 1448; 1449; 1450; 1451; 1452; 1453; 1454; 1455; 1456; 1457; 1458; 1459; 1460; 1461; 1462; 1463; 1464; 1465; 1466; 1467; 1468; 1469; 1470; 1471; 1472; 1473; 1474; 1475; 1476; 1477; 1478; 1479; 1480; 1481; 1482; 1483; 1484; 1485; 1486; 1487; 1488; 1489; 1490; 1491; 1492; 1493; 1494; 1495; 1496; 1497; 1498; 1499; 1500; 1501; 1502; 1503; 1504; 1505; 1506; 1507; 1508; 1509; 1510; 1511; 1512; 1513; 1514; 1515; 1516; 1517; 1518; 1519; 1520; 1521; 1522; 1523; 1524; 1525; 1526; 1527; 1528; 1529; 1530; 1531; 1532; 1533; 1534; 1535; 1536; 1537; 1538; 1539; 1540; 1541; 1542; 1543; 1544; 1545; 1546; 1547; 1548; 1549; 1550; 1551; 1552; 1553; 1554; 1555; 1556; 1557; 1558; 1559; 1560; 1561; 1562; 1563; 1564; 1565; 1566; 1567; 1568; 1569; 1570; 1571; 1572; 1573; 1574; 1575; 1576; 1577; 1578; 1579; 1580; 1581; 1582; 1583; 1584; 1585; 1586; 1587; 1588; 1589; 1590; 1591; 1592; 1593; 1594; 1595; 1596; 1597; 1598; 1599; 1600; 1601; 1602; 1603; 1604; 1605; 1606; 1607; 1608; 1609; 1610; 1611; 1612; 1613; 1614; 1615; 1616; 1617; 1618; 1619; 1620; 1621; 1622; 1623; 1624; 1625; 1626; 1627; 1628; 1629; 1630; 1631; 1632; 1633; 1634; 1635; 1636; 1637; 1638; 1639; 1640; 1641; 1642; 1643; 1644; 1645; 1646; 1647; 1648; 1649; 1650; 1651; 1652; 1653; 1654; 1655; 1656; 1657; 1658; 1659; 1660; 1661; 1662; 1663; 1664; 1665; 1666; 1667; 1668; 1669; 1670; 1671; 1672; 1673; 1674; 1675; 1676; 1677; 1678; 1679; 1680; 1681; 1682; 1683; 1684; 1685; 1686; 1687; 1688; 1689; 1690; 1691; 1692; 1693; 1694; 1695; 1696; 1697; 1698; 1699; 1700; 1701; 1702; 1703; 1704; 1705; 1706; 1707; 1708; 1709; 1710; 1711; 1712; 1713; 1714; 1715; 1716; 1717; 1718; 1719; 1720; 1721; 1722; 1723; 1724; 1725; 1726; 1727; 1728; 1729; 1730; 1731; 1732; 1733; 1734; 1735; 1736; 1737; 1738; 1739; 1740; 1741; 1742; 1743; 1744; 1745; 1746; 1747; 1748; 1749; 1750; 1751; 1752; 1753; 1754; 1755; 1756; 1757; 1758; 1759; 1760; 1761; 1762; 1763; 1764; 1765; 1766; 1767; 1768; 1769; 1770; 1771; 1772; 1773; 1774; 1775; 1776; 1777; 1778; 1779; 1780; 1781; 1782; 1783; 1784; 1785; 1786; 1787; 1788; 1789; 1790; 1791; 1792; 1793; 1794; 1795; 1796; 1797; 1798; 1799; 1800; 1801; 1802; 1803; 1804; 1805; 1806; 1807; 1808; 1809; 1810; 1811; 1812; 1813; 1814; 1815; 1816; 1817; 1818; 1819; 1820; 1821; 1822; 1823; 1824; 1825; 1826; 1827; 1828; 1829; 1830; 1831; 1832; 1833; 1834; 1835; 1836; 1837; 1838; 1839; 1840; 1841; 1842; 1843; 1844; 1845; 1846; 1847; 1848; 1849; 1850; 1851; 1852; 1853; 1854; 1855; 1856; 1857; 1858; 1859; 1860; 1861; 1862; 1863; 1864; 1865; 1866; 1867; 1868; 1869; 1870; 1871; 1872; 1873; 1874; 1875; 1876; 1877; 1878; 1879; 1880; 1881; 1882; 1883; 1884; 1885; 1886; 1887; 1888; 1889; 1890; 1891; 1892; 1893; 1894; 1895; 1896; 1897; 1898; 1899; 1900; 1901; 1902; 1903; 1904; 1905; 1906; 1907; 1908; 1909; 1910; 1911; 1912; 1913; 1914; 1915; 1916; 1917; 1918; 1919; 1920; 1921; 1922; 1923; 1924; 1925; 1926; 1927; 1928; 1929; 1930; 1931; 1932; 1933; 1934; 1935; 1936; 1937; 1938; 1939; 1940; 1941; 1942; 1943; 1944; 1945; 1946; 1947; 1948; 1949; 1950; 1951; 1952; 1953; 1954; 1955; 1956; 1957; 1958; 1959; 1960; 1961; 1962; 1963; 1964; 1965; 1966; 1967; 1968; 1969; 1970; 1971; 1972; 1973; 1974; 1975; 1976; 1977; 1978; 1979; 1980; 1981; 1982; 1983; 1984; 1985; 1986; 1987; 1988; 1989; 1990; 1991; 1992; 1993; 1994; 1995; 1996; 1997; 1998; 1999; 2000; 2001; 2002; 2003; 2004; 2005; 2006; 2007; 2008; 2009; 2010; 2011; 2012; 2013; 2014; 2015; 2016; 2017; 2018; 2019; 2020; 2021; 2022; 2023; 2024; 2025; 2026; 2027; 2028; 2029; 2030; 2031; 2032; 2033; 2034; 2035; 2036; 2037; 2038; 2039; 2040; 2041; 2042; 2043; 2044; 2045; 2046; 2047; 2048; 2049; 2050; 2051; 2052; 2053; 2054; 2055; 2056; 2057; 2058; 2059; 2060; 2061; 2062; 2063; 2064; 2065; 2066; 2067; 2068; 2069; 2070; 2071; 2072; 2073; 2074; 2075; 2076; 2077; 2078; 2079; 2080; 2081; 2082; 2083; 2084; 2085; 2086; 2087; 2088; 2089; 2090; 2091; 2092; 2093; 2094; 2095; 2096; 2097; 2098; 2099; 2100; 2101; 2102; 2103; 2104; 2105; 2106; 2107; 2108; 2109; 2110; 2111; 2112; 2113; 2114; 2115; 2116; 2117; 2118; 2119; 2120; 2121; 2122; 2123; 2124; 2125; 2126; 2127; 2128; 2129; 2130; 2131; 2132; 2133; 2134; 2135; 2136; 2137; 2138; 2139; 2140; 2141; 2142; 2143; 2144; 2145; 2146; 2147; 2148; 2149; 2150; 2151; 2152; 2153; 2154; 2155; 2156; 2157; 2158; 2159; 2160; 2161; 2162; 2163; 2164; 2165; 2166; 2167; 2168; 2169; 2170; 2171; 2172; 2173; 2174; 2175; 2176; 2177; 2178; 2179; 2180; 2181; 2182; 2183; 2184; 2185; 2186; 2187; 2188; 2189; 2190; 2191; 2192; 2193; 2194; 2195; 2196; 2197; 2198; 2199; 2200; 2201; 2202; 2203; 2204; 2205; 2206; 2207; 2208; 2209; 2210; 2211; 2212; 2213; 2214; 2215; 2216;

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announc/>
CC or send an email to license@isb-sib.ch.)

DR EMBL; J04616; J04616.
DR InterPro: IPR000407; GDAI_CD39_NTPASE.
DR PROSITE: PS01238; GDAI_CD39_NTPASE.
DR Hydrolase; Transmembrane; Calcium; Signal.
FT SIGNAL 31 30 POTENTIAL.
FT TRANSHEM 426 446 POTENTIAL.
FT TRANSHEM 151 151 N-LINKED (GLCMAC. .) (POTENTIAL).
FT CMBRDYD 262 262 N-LINKED (GLCMAC. .) (POTENTIAL).
FT CMBRDYD 262 262 N-LINKED (GLCMAC. .) (POTENTIAL).
SQ SEQUENCE 454 AA; 5001 MW; 9058F410A1F5F CRC64;

Query Match 19-88; Score 446.5; DB 1; Length 454;
Best Local Similarity 28.88; Pred. No. 2.6e-28;
Matches 131; Conservative 78; Mismatches 177; Indels 69; Gaps 16;
25 NQVTFEIGFIS---SNCFINVSA---STLYGKFDAGTGRHHY 65
3 KNGHFTPIILAFVPLSLKNNVNAQPIRHLHLSSEHVAIPDAGTSRVNP 62
66 TVTQVQHPDPILEG-SVPDSVGFSLSAFVDQFQAEVTVGLLEKAKDSI PRSHMKKT 124
63 RPEKL-GLPNGINFPYMTAFSLSSAEPDPAANSLPGLQAGVYFQELGSET 121
125 VLVATGALLLEFHEKAKALFEVKEIFR-KSPFLVFKGVSIMDSDEGLVATVNF 183
122 LEACATGALMLKQDAEKILQAVMLVQKSTFSDHQVNTLQDTQGGYMAAINT 181
184 TQGLGHQVQTVGLDGGAGTQITL---PQFKLS-QTPGRLNTPFNSTKLT 239
182 LGNGLQKYSITATIDLGSSVQVAYISNEGFAPAFQEDSGSPYVQGHLSKQNT 241
240 HSYLGFELKARLALGALTECTDGTGFSACLPNLEASWIFGVYVQGHGQVGV 299
300 PEPCVAVLVGVG-KLHQPVEVGRSP---NFCALSGCDQSYGVGVYKVAFGKS- 292
342 HSYLVNTQGLAGRAIFKAPNES---NFCALSGCDQSYGVGVYKVAFGKS- 292
293 ---SWMGRCLTHALINAKNICTGCTGFWGNGGGQDQKIMASFPYDQAOVY 349
343 DYE-KGGLAVDFEPRKAEVCD-NUNFTS---GPEFLMDLYLTALLKDGFS 392
350 DTKPPLQVDTYVLTAAKAVQVNTADISITFPTQVDRNIPYLCMLYEVYLLVD 409
393 P---ADSVLTQLTKYVNI-IFETQWALGATFHLOS 423
410 LNPKHRTIVHDVQYKXNVLUGAMFGCAIDLVES 444

RESULT 9
ID: C4616 STANDARD; PRT: 485 AA.
10 C4616 C4616
11 C4616 C4616
12 C4616 C4616
13 C4616 C4616
14 C4616 C4616
15 C4616 C4616
16 C4616 C4616
17 C4616 C4616
18 C4616 C4616
19 C4616 C4616
20 C4616 C4616
21 C4616 C4616
22 C4616 C4616
23 C4616 C4616
24 C4616 C4616
25 C4616 C4616
26 C4616 C4616
27 C4616 C4616
28 C4616 C4616
29 C4616 C4616
30 C4616 C4616
31 C4616 C4616
32 C4616 C4616
33 C4616 C4616
34 C4616 C4616
35 C4616 C4616
36 C4616 C4616
37 C4616 C4616
38 C4616 C4616
39 C4616 C4616
40 C4616 C4616
41 C4616 C4616
42 C4616 C4616
43 C4616 C4616
44 C4616 C4616
45 C4616 C4616
46 C4616 C4616
47 C4616 C4616
48 C4616 C4616
49 C4616 C4616
50 C4616 C4616
51 C4616 C4616
52 C4616 C4616
53 C4616 C4616
54 C4616 C4616
55 C4616 C4616
56 C4616 C4616
57 C4616 C4616
58 C4616 C4616
59 C4616 C4616
60 C4616 C4616
61 C4616 C4616
62 C4616 C4616
63 C4616 C4616
64 C4616 C4616
65 C4616 C4616
66 C4616 C4616
67 C4616 C4616
68 C4616 C4616
69 C4616 C4616
70 C4616 C4616
71 C4616 C4616
72 C4616 C4616
73 C4616 C4616
74 C4616 C4616
75 C4616 C4616
76 C4616 C4616
77 C4616 C4616
78 C4616 C4616
79 C4616 C4616
80 C4616 C4616
81 C4616 C4616
82 C4616 C4616
83 C4616 C4616
84 C4616 C4616
85 C4616 C4616
86 C4616 C4616
87 C4616 C4616
88 C4616 C4616
89 C4616 C4616
90 C4616 C4616
91 C4616 C4616
92 C4616 C4616
93 C4616 C4616
94 C4616 C4616
95 C4616 C4616
96 C4616 C4616
97 C4616 C4616
98 C4616 C4616
99 C4616 C4616
100 C4616 C4616
101 C4616 C4616
102 C4616 C4616
103 C4616 C4616
104 C4616 C4616
105 C4616 C4616
106 C4616 C4616
107 C4616 C4616
108 C4616 C4616
109 C4616 C4616
110 C4616 C4616
111 C4616 C4616
112 C4616 C4616
113 C4616 C4616
114 C4616 C4616
115 C4616 C4616
116 C4616 C4616
117 C4616 C4616
118 C4616 C4616
119 C4616 C4616
120 C4616 C4616
121 C4616 C4616
122 C4616 C4616
123 C4616 C4616
124 C4616 C4616
125 C4616 C4616
126 C4616 C4616
127 C4616 C4616
128 C4616 C4616
129 C4616 C4616
130 C4616 C4616
131 C4616 C4616
132 C4616 C4616
133 C4616 C4616
134 C4616 C4616
135 C4616 C4616
136 C4616 C4616
137 C4616 C4616
138 C4616 C4616
139 C4616 C4616
140 C4616 C4616
141 C4616 C4616
142 C4616 C4616
143 C4616 C4616
144 C4616 C4616
145 C4616 C4616
146 C4616 C4616
147 C4616 C4616
148 C4616 C4616
149 C4616 C4616
150 C4616 C4616
151 C4616 C4616
152 C4616 C4616
153 C4616 C4616
154 C4616 C4616
155 C4616 C4616
156 C4616 C4616
157 C4616 C4616
158 C4616 C4616
159 C4616 C4616
160 C4616 C4616
161 C4616 C4616
162 C4616 C4616
163 C4616 C4616
164 C4616 C4616
165 C4616 C4616
166 C4616 C4616
167 C4616 C4616
168 C4616 C4616
169 C4616 C4616
170 C4616 C4616
171 C4616 C4616
172 C4616 C4616
173 C4616 C4616
174 C4616 C4616
175 C4616 C4616
176 C4616 C4616
177 C4616 C4616
178 C4616 C4616
179 C4616 C4616
180 C4616 C4616
181 C4616 C4616
182 C4616 C4616
183 C4616 C4616
184 C4616 C4616
185 C4616 C4616
186 C4616 C4616
187 C4616 C4616
188 C4616 C4616
189 C4616 C4616
190 C4616 C4616
191 C4616 C4616
192 C4616 C4616
193 C4616 C4616
194 C4616 C4616
195 C4616 C4616
196 C4616 C4616
197 C4616 C4616
198 C4616 C4616
199 C4616 C4616
200 C4616 C4616
201 C4616 C4616
202 C4616 C4616
203 C4616 C4616
204 C4616 C4616
205 C4616 C4616
206 C4616 C4616
207 C4616 C4616
208 C4616 C4616
209 C4616 C4616
210 C4616 C4616
211 C4616 C4616
212 C4616 C4616
213 C4616 C4616
214 C4616 C4616
215 C4616 C4616
216 C4616 C4616
217 C4616 C4616
218 C4616 C4616
219 C4616 C4616
220 C4616 C4616
221 C4616 C4616
222 C4616 C4616
223 C4616 C4616
224 C4616 C4616
225 C4616 C4616
226 C4616 C4616
227 C4616 C4616
228 C4616 C4616
229 C4616 C4616
230 C4616 C4616
231 C4616 C4616
232 C4616 C4616
233 C4616 C4616
234 C4616 C4616
235 C4616 C4616
236 C4616 C4616
237 C4616 C4616
238 C4616 C4616
239 C4616 C4616
240 C4616 C4616
241 C4616 C4616
242 C4616 C4616
243 C4616 C4616
244 C4616 C4616
245 C4616 C4616
246 C4616 C4616
247 C4616 C4616
248 C4616 C4616
249 C4616 C4616
250 C4616 C4616
251 C4616 C4616
252 C4616 C4616
253 C4616 C4616
254 C4616 C4616
255 C4616 C4616
256 C4616 C4616
257 C4616 C4616
258 C4616 C4616
259 C4616 C4616
260 C4616 C4616
261 C4616 C4616
262 C4616 C4616
263 C4616 C4616
264 C4616 C4616
265 C4616 C4616
266 C4616 C4616
267 C4616 C4616
268 C4616 C4616
269 C4616 C4616
270 C4616 C4616
271 C4616 C4616
272 C4616 C4616
273 C4616 C4616
274 C4616 C4616
275 C4616 C4616
276 C4616 C4616
277 C4616 C4616
278 C4616 C4616
279 C4616 C4616
280 C4616 C4616
281 C4616 C4616
282 C4616 C4616
283 C4616 C4616
284 C4616 C4616
285 C4616 C4616
286 C4616 C4616
287 C4616 C4616
288 C4616 C4616
289 C4616 C4616
290 C4616 C4616
291 C4616 C4616
292 C4616 C4616
293 C4616 C4616
294 C4616 C4616
295 C4616 C4616
296 C4616 C4616
297 C4616 C4616
298 C4616 C4616
299 C4616 C4616
300 C4616 C4616
301 C4616 C4616
302 C4616 C4616
303 C4616 C4616
304 C4616 C4616
305 C4616 C4616
306 C4616 C4616
307 C4616 C4616
308 C4616 C4616
309 C4616 C4616
310 C4616 C4616
311 C4616 C4616
312 C4616 C4616
313 C4616 C4616
314 C4616 C4616
315 C4616 C4616
316 C4616 C4616
317 C4616 C4616
318 C4616 C4616
319 C4616 C4616
320 C4616 C4616
321 C4616 C4616
322 C4616 C4616
323 C4616 C4616
324 C4616 C4616
325 C4616 C4616
326 C4616 C4616
327 C4616 C4616
328 C4616 C4616
329 C4616 C4616
330 C4616 C4616
331 C4616 C4616
332 C4616 C4616
333 C4616 C4616
334 C4616 C4616
335 C4616 C4616
336 C4616 C4616
337 C4616 C4616
338 C4616 C4616
339 C4616 C4616
340 C4616 C4616
341 C4616 C4616
342 C4616 C4616
343 C4616 C4616
344 C4616 C4616
345 C4616 C4616
346 C4616 C4616
347 C4616 C4616
348 C4616 C4616
349 C4616 C4616
350 C4616 C4616
351 C4616 C4616
352 C4616 C4616
353 C4616 C4616
354 C4616 C4616
355 C4616 C4616
356 C4616 C4616
357 C4616 C4616
358 C4616 C4616
359 C4616 C4616
360 C4616 C4616
361 C4616 C4616
362 C4616 C4616
363 C4616 C4616
364 C4616 C4616
365 C4616 C4616
366 C4616 C4616
367 C4616 C4616
368 C4616 C4616
369 C4616 C4616
370 C4616 C4616
371 C4616 C4616
372 C4616 C4616
373 C4616 C4616
374 C4616 C4616
375 C4616 C4616
376 C4616 C4616
377 C4616 C4616
378 C4616 C4616
379 C4616 C4616
380 C4616 C4616
381 C4616 C4616
382 C4616 C4616
383 C4616 C4616
384 C4616 C4616
385 C4616 C4616
386 C4616 C4616
387 C4616 C4616
388 C4616 C4616
389 C4616 C4616
390 C4616 C4616
391 C4616 C4616
392 C4616 C4616
393 C4616 C4616
394 C4616 C4616
395 C4616 C4616
396 C4616 C4616
397 C4616 C4616
398 C4616 C4616
399 C4616 C4616
400 C4616 C4616
401 C4616 C4616
402 C4616 C4616
403 C4616 C4616
404 C4616 C4616
405 C4616 C4616
406 C4616 C4616
407 C4616 C4616
408 C4616 C4616
409 C4616 C4616
410 C4616 C4616
411 C4616 C4616
412 C4616 C4616
413 C4616 C4616
414 C4616 C4616
415 C4616 C4616
416 C4616 C4616
417 C4616 C4616
418 C4616 C4616
419 C4616 C4616
420 C4616 C4616
421 C4616 C4616
422 C4616 C4616
423 C4616 C4616
424 C4616 C4616
425 C4616 C4616
426 C4616 C4616
427 C4616 C4616
428 C4616 C4616
429 C4616 C4616
430 C4616 C4616
431 C4616 C4616
432 C4616 C4616
433 C4616 C4616
434 C4616 C4616
435 C4616 C4616
436 C4616 C4616
437 C4616 C4616
438 C4616 C4616
439 C4616 C4616
440 C4616 C4616
441 C4616 C4616
442 C4616 C4616
443 C4616 C4616
444 C4616 C4616
445 C4616 C4616
446 C4616 C4616
447 C4616 C4616
448 C4616 C4616
449 C4616 C4616
450 C4616 C4616
451 C4616 C4616
452 C4616 C4616
453 C4616 C4616
454 C4616 C4616
455 C4616 C4616
456 C4616 C4616
457 C4616 C4616
458 C4616 C4616
459 C4616 C4616
460 C4616 C4616
461 C4616 C4616
462 C4616 C4616
463 C4616 C4616
464 C4616 C4616
465 C4616 C4616
466 C4616 C4616
467 C4616 C4616
468 C4616 C4616
469 C4616 C4616
470 C4616 C4616
471 C4616 C4616
472 C4616 C4616
473 C4616 C4616
474 C4616 C4616
475 C4616 C4616
476 C4616 C4616
477 C4616 C4616
478 C4616 C4616
479 C4616 C4616
480 C4616 C4616
481 C4616 C4616
482 C4616 C4616
483 C4616 C4616
484 C4616 C4616
485 C4616 C4616
486 C4616 C4616
487 C4616 C4616
488 C4616 C4616
489 C4616 C4616
490 C4616 C4616
491 C4616 C4616
492 C4616 C4616
493 C4616 C4616
494 C4616 C4616
495 C4616 C4616
496 C4616 C4616
497 C4616 C4616
498 C4616 C4616
499 C4616 C4616
500 C4616 C4616
501 C4616 C4616
502 C4616 C4616
503 C4616 C4616
504 C4616 C4616
505 C4616 C4616
506 C4616 C4616
507 C4616 C4616
508 C4616 C4616
509 C4616 C4616
510 C4616 C4616
511 C4616 C4616
512 C4616 C4616
513 C4616 C4616
514 C4616 C4616
515 C4616 C4616
516 C4616 C4616
517 C4616 C4616
518 C4616 C4616
519 C4616 C4616
520 C4616 C4616
521 C4616 C4616
522 C4616 C4616
523 C4616 C4616
524 C4616 C4616
525 C4616 C4616
526 C4616 C4616
527 C4616 C4616
528 C4616 C4616
529 C4616 C4616
530 C4616 C4616
531 C4616 C4616
532 C4616 C4616
533 C4616 C4616
534 C4616 C4616
535 C4616 C4616
536 C4616 C4616
537 C4616 C4616
538 C4616 C4616
539 C4616 C4616
540 C4616 C4616
541 C4616 C4616
542 C4616 C4616
543 C4616 C4616
544 C4616 C4616
545 C4616 C4616
546 C4616 C4616
547 C4616 C4616
548 C4616 C4616
549 C4616 C4616
550 C4616 C4616
551 C4616 C4616
552 C4616 C4616
553 C4616 C4616
554 C4616 C4616
555 C4616 C4616
556 C4616 C4616
557 C4616 C4616
558 C4616 C4616
559 C4616 C4616
560 C4616 C4616
561 C4616 C4616
562 C4616 C4616
563 C4616 C4616
564 C4616 C4616
565 C4616 C4616
566 C4616 C4616
567 C4616 C4616
568 C4616 C4616
569 C4616 C4616
570 C4616 C4616
571 C4616 C4616
572 C4616 C4616
573 C4616 C4616
574 C4616 C4616
575 C4616 C4616
576 C4616 C4616
577 C4616 C4616
578 C4616 C4616
579 C4616 C4616
580 C4616 C4616
581 C4616 C4616
582 C4616 C4616
583 C4616 C4616
584 C4616 C4616
585 C4616 C4616
586 C4616 C4616
587 C4616 C4616
588 C4616 C4616
589 C4616 C4616
590 C4616 C4616
591 C4616 C4616
592 C4616 C4616
593 C4616 C4616
594 C4616 C4616
595 C4616 C4616
596 C4616 C4616
597 C4616 C4616
598 C4616 C4616
599 C4616 C4616
600 C4616 C4616
601 C4616 C4616
602 C4616 C4616
603 C4616 C4616
604 C4616 C4616
605 C4616 C4616
606 C4616 C4616
607 C4616 C4616
608 C4616 C4616
609 C4616 C4616
610 C4616 C4616
611 C4616 C4616
612 C4616 C4616
613 C4616 C4616
614 C4616 C4616
615 C4616 C4616
616 C4616 C4616
617 C4616 C4616
618 C4616 C4616
619 C4616 C4616
620 C4616 C4616
621 C4616 C4616
622 C4616 C4616
623 C4616 C4616
624 C4616 C4616
625 C4616 C4616
626 C4616 C4616
627 C4616 C4616
628 C4616 C4616
629 C4616 C4616
630 C4616 C4616
631 C4616 C4616
632 C4616 C4616
633 C4616 C4616
634 C4616 C4616
635 C4616 C4616
636 C4616 C4616
637 C4616 C4616
638 C4616 C4616
639 C4616 C4616
640 C4616 C4616
641 C4616 C4616
642 C4616 C4616
643 C4616 C4616
644 C4616 C4616
645 C4616 C4616
646 C4616 C4616
647 C4616 C4616
648 C4616 C4616
649 C4616 C4616
650 C4616 C4616
651 C4616 C4616
652 C4616 C4616
653 C4616 C4616
654 C4616 C4616
655 C4616 C4616
656 C4616 C4616
657 C4616 C4616
658 C4616 C4616
659 C4616 C4616
660 C4616 C4616
661 C4616 C4616
662 C4616 C4616
663 C4616 C4616
664 C4616 C4616
665 C4616 C4616
666 C4616 C4616
667 C4616 C4616
668 C4616 C4616
669 C4616 C4616
670 C4616 C4616
671 C4616 C4616
672 C4616 C4616
673 C4616 C4616
674 C4616 C4616
675 C4616 C4616
676 C4616 C4616
677 C4616 C4616
678 C4616 C4616
679 C4616 C4616
680 C4616 C4616
681 C4616 C4616
682 C4616 C4616
683 C4616 C4616
684 C4616 C4616
685 C4616 C4616
686 C4616 C4616
687 C4616 C4616
688 C4616 C4616
689 C4616 C4616
690 C4616 C4616
691 C4616 C4616
692 C4616 C4616
693 C4616 C4616
694 C4616 C4616
695 C4616 C4616
696 C4616 C4616
697 C4616 C4616
698 C4616 C4616
699 C4616 C4616
700 C4616 C4616
701 C4616 C4616
702 C4616 C4616
703 C4616 C4616
704 C4616 C4616
705 C4616 C4616
706 C4616 C4616
707 C4616 C4616
708 C4616 C4616
709 C4616 C4616
710 C4616 C4616
711 C4616 C4616
712 C4616 C4616
713 C4616 C4616
714 C4616 C4616
715 C4616 C4616
716 C4616 C4616
717 C4616 C4616
718 C4616 C4616
719 C4616 C4616
720 C4616 C4616
721 C4616 C4616
722 C4616 C4616
723 C4616 C4616
724 C4616 C4616
725 C4616 C4616
726 C4616 C4616
727 C4616 C4616
728 C4616 C4616
729 C4616 C4616
730 C4616 C4616
731 C4616 C4616
732 C4616 C4616
733 C4616 C4616
734 C4616 C4616
735 C4616 C4616
736 C4616 C4616
737 C4616 C4616
738 C4616 C4616
739 C4616 C4616
740 C4616 C4616
741 C4616 C4616
742 C4616 C4616
743 C4616 C4616
744 C4616 C4616
745 C4616 C4616
746 C4616 C4616
747 C4616 C4616
748 C4616 C4616
749 C4616 C4616
750 C4616 C4616
751 C4


```

11  LKATVFIIILAILLADNVKPL.....PRTKGLVFDAGSTPRSHVYVMPAD 62
QY 70  KMEGQDILLEGVDFVSGVAGVDFVQKGAETVQGLELVKARDISPRHVKATPVILKA 129
DB 63  KENGTVQVQVRESCITVNGSGISVADYDAGAKSLKPLCDANAVIVQVQDQPTFLGA 122
QY 130  TAGLRLPLPH.....KAVALLKEVKEIPKPSFPLVPGVSVIMQSGDGLIAWTVNLTQ 186
DB 123  TAGMELLRLQNSSTAAQVAFVSAKIREP...VDFRQAGILITONEBSGFGNITWYLLT 180
QY 187  L.....HGHQSGVFTVLIDLGASTQITELPQEKTLQTPRGVLSFENFENSTYK 236
DB 181  LKRFSEFAGNEHPONTEVGLADILGASQTITQEQV...TIEDNTSVL...FRAGTNTS 236
QY 237  LYTHSYVGLGLVGLAARLALTALETFCTGHTFSCPLPLKLEKISFQGVYVQNGOR- 295
DB 237  LYTHSYVLCVCTQASKEMLAALHODGSVQNI SHECPFK.....GKRLI 280
QY 296  .....GKQVCFQY.....ABUAVVR.....GKRLI 317
DB 281  ITTATISVLCVCTPFSKLSPAQILVTGTGPAACFTALLALPNLTGNACRTQCFGVYQ 340
QY 318  PRVQVSGTSTAYS...YVYDRA.....VQTDMDKY...ENGKILYVDFPERKAEVC 363
DB 341  PP...VRQGFQAFAGVITFSTFSLNTQCSLSHVNATWDFVNNSELVETPKNK... 394
QY 364  DNLEWTFSPFPCNDGLSYTVALKGQFPAQST...VLGLPKKVNINIFWALQNTFL 420
DB 395  EAGHTY.....CVGLYLVLTVLVDGYVADHTNHSIFSQAGNADIGWLGPNLNL 446

RESULT 12
VNDL YEAST
ID VNDL YEAST STANDARD; PRT; 630 AA.
AC P40009; 1986 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine
DE diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
DE VNDL OR0015M
OS Saccharomyces cerevisiae (Baker's Yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX Eukaryotes; Saccharomycotinae; Saccharomycos.
ON NCBI TaxID:4932.
[1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
AC MENLNE93160091; PubMed10409709;
Gao X.D., Kaigocodov V., Jigami Y.,
Gao X.D., a homologue of Gdali, encodes membrane-bound apyrase required
for Golgi N- and O-glycosylation in Saccharomyces cerevisiae.;
[2] Biol. Chem. 274:21450-21456 (1999).
SEQUENCE FROM N.A.
AC STAIN5288C / AB977;
Barnett J.,
Dierich P.S., Walligan J.T., Hennessy K.M., Yellon M.A., Allen F.,
Aravio R., Aviles E., Berno A., Brennan T., Carpenter U., Chan E.,
Chen J.M., Chung E., Duncan M., Guman E., Hartell G.,
Hunkeler-Smith S., Ryan R.W., Kayser A., Kopp C., Lashkari D., Low H.,
Mannervik B., Marmè D., Marmè D., Marmè D., Marmè D., Marmè D.,
Oh C., Patel F.X., Roberts D., Sahi P., Schram S., Shogren F.,
Smith V., Taylor P., Wei Y., Boettstein D., Davis R.N.;
[1] The nucleotide sequence of Saccharomyces cerevisiae chromosome V.;
[2] FUNCTION: CATALYZES THE HYDROLYSIS OF PHOSPHORIBOSYL DIPHOSPHATE
[3] NUCLEOSIDE TRI- AND DI-PHOSPHATES. HAS EQUIVALENT HIGH ACTIVITY TOWARD
ADP/ATP, GDP/GTP, AND UDP/UTP AND APPROXIMATELY 50% LESS TOWARD
ADP/ATP AND THIAMINE PHOSPHATES. HAS NO ACTIVITY TOWARD GMP.
REQUIRED FOR GOLGI GLYCOSYLATION AND CELL WALL INTEGRITY.

```

```

CC CC CATALYTIC ACTIVITY: ATP + 2 H(2O) = AMP + 2 phosphate.
CC CC ENZYME CLASSIFICATION: EC 3.6.1.5
CC CC SIMILARITY: BELONGS TO THE GdAL / CD39 INTRAFAMILY.
CC CC
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the European Bioinformatics Institute and the Swiss Institute of
CC CC Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announcements/
CC CC
CC CC EMBL; AF203695; AAF17573.1;
CC CC EMBL; U18778; M864538.1;
CC CC SDD; S0000807; VNDL.
CC CC GO: 0006486; P: protein amino acid glycosylation; IMP.
CC CC InterPro; I000407; GdAL_CD39_MTPase.
CC CC PROSITE; PS01238; GdAL_CD39_MTPase; 1.
CC CC Hydrolase; Transmembrane; Golgi; stack.
CC CC DOMAIN 501 500 LUMENAL (POTENTIAL).
CC CC TRANSHEM 501 517 POTENTIAL.
CC CC CDS 517 517 POTENTIAL.
CC CC SEQUENCE 630 AA; 71851 MW; 02F8D2A78212544 CRC64;

Query Match 16.5%; Score 372; DB 1; Length 630.
Similarity 16.4%; Protein No. 98.
Matches 117; Conservative 71; Mismatch 165; Gaps 17;

QY 49  GYIMDADGTRTHVYTF.....VQNMQLPILLEG--VDFSVPLGSA 92
DB 10  RYIVLVSSGSHVHFVQVTSLLHNTKQSGILASVHIQKQWTF-KLNPGRS 68
QY 93  FVDQPKQAGT-VQGLELVKARDISPRHVKATPVILKATGLLPEKAKALLFEV-KE 150
DB 69  FKKRPDPNVKSHIFLLDPANHIFEDHNSCVFQKAKGLLPQDQSGILQGLG 128
QY 151  FPKSPPLVP--KGSVITMVGSDGLIAWTVNLTQKHQEQE-----TVGLDGLGA 203
DB 129  LKHPALFVDECAQQLVDIGETGLYGLGLATLGHFNDVPEVSDVTFPGHMDGA 188
QY 204  STQITLTPQPEKTLK.....STQGVYTFSEPMSTVLYSLGRLKAKRL 252
DB 183  STQITLTPQPEKTLK.....STQGVYTFSEPMSTVLYSLGRLKAKRL 252
QY 253  ATGALFAGSGEINAEHRDDINTIFLNSQDLMQVDFD-----WLPFANQAR 241
DB 189  ATGALFAGSGEINAEHRDDINTIFLNSQDLMQVDFD-----WLPFANQAR 241
QY 243  RYLAQLLNTLFNTYDNDSTFNLNDFCFRSGSTDFEFQTFHAGSGYBCKT 301
DB 242  RYLAQLLNTLFNTYDNDSTFNLNDFCFRSGSTDFEFQTFHAGSGYBCKT 301
QY 302  PCYAEVIR.....VVRKLPQEQE-VQSGSFASVYVTRAVDTMDYKEGGLAV 352
DB 302  PCYAEVIR.....VVRKLPQEQE-VQSGSFASVYVTRAVDTMDYKEGGLAV 352
QY 303  STYPLPLKNNVCDDECFCLVGHVAPRIDFANDFVITGSETWYANDV--FLGGEVNF 357
DB 303  STYPLPLKNNVCDDECFCLVGHVAPRIDFANDFVITGSETWYANDV--FLGGEVNF 357
QY 353  DKFSKAEKAEV.....LENVTSQ-----SPEL--CDGLSVITALKQSGFA---- 394
DB 353  DKFSKAEKAEV.....LENVTSQ-----SPEL--CDGLSVITALKQSGFA---- 394
QY 358  DKFSKAEKAEV.....LENVTSQ-----SPEL--CDGLSVITALKQSGFA---- 394
DB 358  DKFSKAEKAEV.....LENVTSQ-----SPEL--CDGLSVITALKQSGFA---- 394
QY 395  -----DSTVQLKPKNNITGTMALG 415
DB 395  -----DSTVQLKPKNNITGTMALG 415
QY 418  DARNVNDPLRFQSVENVEEELSVTLG 444
DB 418  DARNVNDPLRFQSVENVEEELSVTLG 444

RESULT 13
ENPLI MOUSE
ID ENPLI MOUSE STANDARD; PRT; 510 AA.
AC P55772; 1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPdase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell

```


D6	383	TLV,LOQ,EDD,LC-RET,OPK,NK,NTQ,SL,NV,OPP,HP,NBF,GSF,TCZD,441	TLV,LOQ,EDD,LC-RET,OPK,NK,NTQ,SL,NV,OPP,HP,NBF,GSF,TCZD,441
Qy	340	DM,IEKGG,LLV,EFER,RE,RYCVD,-----LENTFSG,-----SP,LCND,USJ,384	DM,IEKGG,LLV,EFER,RE,RYCVD,-----LENTFSG,-----SP,LCND,USJ,384
Qy	442	-----LNMGGY,NM,AF,QAADY,CAT,KS,LR,ER,FGL,YASH,AD,HL,RY,CT,SG,NM,FE,497	-----LNMGGY,NM,AF,QAADY,CAT,KS,LR,ER,FGL,YASH,AD,HL,RY,CT,SG,NM,FE,497
Qy	385	ALL,KD,SE,PD,OS,-----TL,GT,EL,KNN,ET,FW,GA,TH,419	ALL,KD,SE,PD,OS,-----TL,GT,EL,KNN,ET,FW,GA,TH,419
D6	498	EV,PH,GF,SE,FPV,TK,SL,TAL,OV,DK,-----BV,MT,GL,TH,533	EV,PH,GF,SE,FPV,TK,SL,TAL,OV,DK,-----BV,MT,GL,TH,533

Search completed: November 13, 2003, 06:17:32
Job time : 22 secs

Query Match	16.08;	Score 360.51;	DB 1;	Length 613;
Best Local Similarity	34.48;	Pred. No. 3.2e-21;		
Matches 127;	Conservative 77;	Mismatches 185;	Indels 131;	Gaps 21;
QY	11	MLVSGVCSANE-----HNOHWTE-----GIFLSKSTFNW-----SASTLVGNF 53		
DD	34	IVTISLAAALSYLGVSVTHSKYKMSKDKKFKRTARTVDVATQTSNPNVGVIG 93		
QY	54	DAGSTGTRTHVTFVQMGQGLPFL-----GEVDFKVGSLFAVPOQKQAFV 104		
DD	104	DCGSLGSLVTFVFNHNGNDLHDDIQMDQKQVFNWMLKTSFSAFPEKVDYI 153		
QY	105	EGELWAKDSIFRSHKHKTFVULKATGAGLLPEKAKALLFVKELISF-----ELVP 160		
DD	154	STLSSFAEHLVPAHKAHAFKFFVLTCAHMLVFEQKQATL-----EDLDTFPHVDFES 210		
QY	161	KGSVITMGSGEDGLAMVAVFUTGQLGH-----SDEVTGCT 197		
DD	211	DSNARYTSGQVFAWGMIGVIFGFRPH-----FHEEDFAVWVTFQSSSAVACVAGTA 269		
QY	198	LDLGGASTQTFVLTQ-----FENLTGPTPGVLTFSFM-----FNSYKALVTHSYLGG 246		
DD	270	LKNGVSTQVATVEVPTVSPASQCEQVAMLVKMLHCCDQVQVTHVAVVATFLGG 329		
QY	247	LKAAALA-----TLGALETGTGHTFSACLPMLKBAEMTFGVQKGVGN 293		
DD	330	GNIAKQVRFVFASTVQNNHKGQGLTFDPAFLDPLCLDKTQK-----TQNGQ 382		
QY	394	Q-----EGEFGFCAVEMLVKSHG-----PEHGEFGSVFASYVDAVNT 339		

GenCass version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 06:08:47 : Search time 49 Seconds

(Without alignments)
1386.428 Million cell updates/sec

Title: US-09-905-744b-6
Perfect score: 2250
Sequence: 1 MATSGTGVFNVLWSCVSA.....ETGNALGATPHLLASLGTSIH 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	2250	100.0	428	21	AAV44849	Human CD39-L4 prot
2	2250	100.0	428	21	AAV72238	Human CD39 like pr
3	2250	100.0	428	21	AAV72243	Human CD39 like pr
4	2250	100.0	428	21	AAV44849	Human CD39-L4 prot
5	2250	100.0	428	21	AAV72240	Human CD39-L4 prot
6	2250	99.3	428	21	AAV72240	Human CD39-L4 prot
7	2104	91.5	405	21	AAV44851	Human CD39-L66 pr
8	2104	91.5	405	22	AAV72239	Human CD39 like pr
9	1822.5	81.4	465	23	AAV13694	Mouse CD39L4 prot

Human colon cancer
Human CD39L2 prot
Human CD39-L4 pr
Human NSC
Protein of NOVA 15
Human polypeptide,
Protein of NOVA 15
Human CD39-L4 pr
Mature human CD39
Drosophila melanog
Drosophila melanog
Protein encoded by
Human CD39-L4 pr
Human CD39-L4 pr
NP46 root lectin.
Human CD39-L4 pr
DBX oligonucleotide
NP46 root lectin.
Dolichos biflorus
Human CD39-L4 pr
Human CD39-L4 pr
Arabidopsis thalia
Human membrane gpa
Human CD39-L4 pr
Human PRO5775 prot
Human secreted/ttra
Novel human secret
Human secreted/ttra
Human secreted/ttra
Human PRO polypept
Human secreted/ttra
Human PRO polypept
Human PRO polypept
Human PRO polypept
Protein encoded by

ALIGNMENTS

RESULT 1
ID AAV44849
ID AAV44849 standard; Protein: 428 AA.

AC AAV44849;
XX AAV44849 (first entry)

DE 18-MAY-2000 (first entry)
XX Human CD39-L4 protein.

DE Human CD39-L4 protein.
XX CD39-L4, human, glycosyl, nucleoside diphosphatase, NPasep, treatment;
XX ATP diphosphatase, ATPasep, nucleoside diphosphatase, NPasep, treatment;
XX platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
XX cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
XX molecular weight marker; nutritional supplement; tumour; prevention;
XX drug targeting; NPasep Conserved Region, AC.

OS Homo sapiens.
XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

XX Key
XX Key
XX Key

RESULT 4

1D AAE19883 standard; Protein; 428 AA.

AC AAE19883;
 DT 18-JUN-2002 (first entry)
 XX Human CD39L4 protein.

XX Human CD39-like protein, CD39L4 protein; therapy; immune deficiency;
 XX autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 XX rheumatoid arthritis; autoimmunity; allergic reaction; asthma;
 XX insulin dependent diabetes mellitus; pericardial disease; osteoporosis;
 XX Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 XX nervous system disease; nerve injury; ischemia-reperfusion injury;
 XX endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 XX dermatological; immunosuppressive; vulvar; neoplastic; anticonvulsant;
 XX antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

XX Homo sapiens.
 CC US6350447-B1.
 XX 26-FEB-2002.
 XX 29-JAN-1999; 99US-0240639.
 XX 29-JAN-1999; 99US-0240639.
 XX (HVSE-) HVSEQ INC.
 XX Chadwick BP, Frischauf A;
 XX N-PSDB; RAD31695.

XX An isolated polypeptide with phosphodiesterase activity, designated
 CC CD39L2, useful to identify other proteins with which binding occurs or
 CC identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
 CC sclerosis and osteoporosis.
 CC Example; Fig 7; 10pp; English.

XX The present invention relates to novel proteins with phosphodiesterase
 CC activity, encoding such proteins. CD39L2, CD39L3, CD39L4, CD39L5, CD39L6, CD39L7, CD39L8, CD39L9, CD39L10, CD39L11, CD39L12, CD39L13, CD39L14, CD39L15, CD39L16, CD39L17, CD39L18, CD39L19, CD39L20, CD39L21, CD39L22, CD39L23, CD39L24, CD39L25, CD39L26, CD39L27, CD39L28, CD39L29, CD39L30, CD39L31, CD39L32, CD39L33, CD39L34, CD39L35, CD39L36, CD39L37, CD39L38, CD39L39, CD39L40, CD39L41, CD39L42, CD39L43, CD39L44, CD39L45, CD39L46, CD39L47, CD39L48, CD39L49, CD39L50, CD39L51, CD39L52, CD39L53, CD39L54, CD39L55, CD39L56, CD39L57, CD39L58, CD39L59, CD39L60, CD39L61, CD39L62, CD39L63, CD39L64, CD39L65, CD39L66, CD39L67, CD39L68, CD39L69, CD39L70, CD39L71, CD39L72, CD39L73, CD39L74, CD39L75, CD39L76, CD39L77, CD39L78, CD39L79, CD39L80, CD39L81, CD39L82, CD39L83, CD39L84, CD39L85, CD39L86, CD39L87, CD39L88, CD39L89, CD39L90, CD39L91, CD39L92, CD39L93, CD39L94, CD39L95, CD39L96, CD39L97, CD39L98, CD39L99, CD39L100, CD39L101, CD39L102, CD39L103, CD39L104, CD39L105, CD39L106, CD39L107, CD39L108, CD39L109, CD39L110, CD39L111, CD39L112, CD39L113, CD39L114, CD39L115, CD39L116, CD39L117, CD39L118, CD39L119, CD39L120, CD39L121, CD39L122, CD39L123, CD39L124, CD39L125, CD39L126, CD39L127, CD39L128, CD39L129, CD39L130, CD39L131, CD39L132, CD39L133, CD39L134, CD39L135, CD39L136, CD39L137, CD39L138, CD39L139, CD39L140, CD39L141, CD39L142, CD39L143, CD39L144, CD39L145, CD39L146, CD39L147, CD39L148, CD39L149, CD39L150, CD39L151, CD39L152, CD39L153, CD39L154, CD39L155, CD39L156, CD39L157, CD39L158, CD39L159, CD39L160, CD39L161, CD39L162, CD39L163, CD39L164, CD39L165, CD39L166, CD39L167, CD39L168, CD39L169, CD39L170, CD39L171, CD39L172, CD39L173, CD39L174, CD39L175, CD39L176, CD39L177, CD39L178, CD39L179, CD39L180, CD39L181, CD39L182, CD39L183, CD39L184, CD39L185, CD39L186, CD39L187, CD39L188, CD39L189, CD39L190, CD39L191, CD39L192, CD39L193, CD39L194, CD39L195, CD39L196, CD39L197, CD39L198, CD39L199, CD39L200, CD39L201, CD39L202, CD39L203, CD39L204, CD39L205, CD39L206, CD39L207, CD39L208, CD39L209, CD39L210, CD39L211, CD39L212, CD39L213, CD39L214, CD39L215, CD39L216, CD39L217, CD39L218, CD39L219, CD39L220, CD39L221, CD39L222, CD39L223, CD39L224, CD39L225, CD39L226, CD39L227, CD39L228, CD39L229, CD39L230, CD39L231, CD39L232, CD39L233, CD39L234, CD39L235, CD39L236, CD39L237, CD39L238, CD39L239, CD39L240, CD39L241, CD39L242, CD39L243, CD39L244, CD39L245, CD39L246, CD39L247, CD39L248, CD39L249, CD39L250, CD39L251, CD39L252, CD39L253, CD39L254, CD39L255, CD39L256, CD39L257, CD39L258, CD39L259, CD39L260, CD39L261, CD39L262, CD39L263, CD39L264, CD39L265, CD39L266, CD39L267, CD39L268, CD39L269, CD39L270, CD39L271, CD39L272, CD39L273, CD39L274, CD39L275, CD39L276, CD39L277, CD39L278, CD39L279, CD39L280, CD39L281, CD39L282, CD39L283, CD39L284, CD39L285, CD39L286, CD39L287, CD39L288, CD39L289, CD39L290, CD39L291, CD39L292, CD39L293, CD39L294, CD39L295, CD39L296, CD39L297, CD39L298, CD39L299, CD39L300, CD39L301, CD39L302, CD39L303, CD39L304, CD39L305, CD39L306, CD39L307, CD39L308, CD39L309, CD39L310, CD39L311, CD39L312, CD39L313, CD39L314, CD39L315, CD39L316, CD39L317, CD39L318, CD39L319, CD39L320, CD39L321, CD39L322, CD39L323, CD39L324, CD39L325, CD39L326, CD39L327, CD39L328, CD39L329, CD39L330, CD39L331, CD39L332, CD39L333, CD39L334, CD39L335, CD39L336, CD39L337, CD39L338, CD39L339, CD39L340, CD39L341, CD39L342, CD39L343, CD39L344, CD39L345, CD39L346, CD39L347, CD39L348, CD39L349, CD39L350, CD39L351, CD39L352, CD39L353, CD39L354, CD39L355, CD39L356, CD39L357, CD39L358, CD39L359, CD39L360, CD39L361, CD39L362, CD39L363, CD39L364, CD39L365, CD39L366, CD39L367, CD39L368, CD39L369, CD39L370, CD39L371, CD39L372, CD39L373, CD39L374, CD39L375, CD39L376, CD39L377, CD39L378, CD39L379, CD39L380, CD39L381, CD39L382, CD39L383, CD39L384, CD39L385, CD39L386, CD39L387, CD39L388, CD39L389, CD39L390, CD39L391, CD39L392, CD39L393, CD39L394, CD39L395, CD39L396, CD39L397, CD39L398, CD39L399, CD39L400, CD39L401, CD39L402, CD39L403, CD39L404, CD39L405, CD39L406, CD39L407, CD39L408, CD39L409, CD39L410, CD39L411, CD39L412, CD39L413, CD39L414, CD39L415, CD39L416, CD39L417, CD39L418, CD39L419, CD39L420, CD39L421, CD39L422, CD39L423, CD39L424, CD39L425, CD39L426, CD39L427, CD39L428, CD39L429, CD39L430, CD39L431, CD39L432, CD39L433, CD39L434, CD39L435, CD39L436, CD39L437, CD39L438, CD39L439, CD39L440, CD39L441, CD39L442, CD39L443, CD39L444, CD39L445, CD39L446, CD39L447, CD39L448, CD39L449, CD39L450, CD39L451, CD39L452, CD39L453, CD39L454, CD39L455, CD39L456, CD39L457, CD39L458, CD39L459, CD39L460, CD39L461, CD39L462, CD39L463, CD39L464, CD39L465, CD39L466, CD39L467, CD39L468, CD39L469, CD39L470, CD39L471, CD39L472, CD39L473, CD39L474, CD39L475, CD39L476, CD39L477, CD39L478, CD39L479, CD39L480, CD39L481, CD39L482, CD39L483, CD39L484, CD39L485, CD39L486, CD39L487, CD39L488, CD39L489, CD39L490, CD39L491, CD39L492, CD39L493, CD39L494, CD39L495, CD39L496, CD39L497, CD39L498, CD39L499, CD39L500, CD39L501, CD39L502, CD39L503, CD39L504, CD39L505, CD39L506, CD39L507, CD39L508, CD39L509, CD39L510, CD39L511, CD39L512, CD39L513, CD39L514, CD39L515, CD39L516, CD39L517, CD39L518, CD39L519, CD39L520, CD39L521, CD39L522, CD39L523, CD39L524, CD39L525, CD39L526, CD39L527, CD39L528, CD39L529, CD39L530, CD39L531, CD39L532, CD39L533, CD39L534, CD39L535, CD39L536, CD39L537, CD39L538, CD39L539, CD39L540, CD39L541, CD39L542, CD39L543, CD39L544, CD39L545, CD39L546, CD39L547, CD39L548, CD39L549, CD39L550, CD39L551, CD39L552, CD39L553, CD39L554, CD39L555, CD39L556, CD39L557, CD39L558, CD39L559, CD39L560, CD39L561, CD39L562, CD39L563, CD39L564, CD39L565, CD39L566, CD39L567, CD39L568, CD39L569, CD39L570, CD39L571, CD39L572, CD39L573, CD39L574, CD39L575, CD39L576, CD39L577, CD39L578, CD39L579, CD39L580, CD39L581, CD39L582, CD39L583, CD39L584, CD39L585, CD39L586, CD39L587, CD39L588, CD39L589, CD39L590, CD39L591, CD39L592, CD39L593, CD39L594, CD39L595, CD39L596, CD39L597, CD39L598, CD39L599, CD39L600, CD39L601, CD39L602, CD39L603, CD39L604, CD39L605, CD39L606, CD39L607, CD39L608, CD39L609, CD39L610, CD39L611, CD39L612, CD39L613, CD39L614, CD39L615, CD39L616, CD39L617, CD39L618, CD39L619, CD39L620, CD39L621, CD39L622, CD39L623, CD39L624, CD39L625, CD39L626, CD39L627, CD39L628, CD39L629, CD39L630, CD39L631, CD39L632, CD39L633, CD39L634, CD39L635, CD39L636, CD39L637, CD39L638, CD39L639, CD39L640, CD39L641, CD39L642, CD39L643, CD39L644, CD39L645, CD39L646, CD39L647, CD39L648, CD39L649, CD39L650, CD39L651, CD39L652, CD39L653, CD39L654, CD39L655, CD39L656, CD39L657, CD39L658, CD39L659, CD39L660, CD39L661, CD39L662, CD39L663, CD39L664, CD39L665, CD39L666, CD39L667, CD39L668, CD39L669, CD39L670, CD39L671, CD39L672, CD39L673, CD39L674, CD39L675, CD39L676, CD39L677, CD39L678, CD39L679, CD39L680, CD39L681, CD39L682, CD39L683, CD39L684, CD39L685, CD39L686, CD39L687, CD39L688, CD39L689, CD39L690, CD39L691, CD39L692, CD39L693, CD39L694, CD39L695, CD39L696, CD39L697, CD39L698, CD39L699, CD39L700, CD39L701, CD39L702, CD39L703, CD39L704, CD39L705, CD39L706, CD39L707, CD39L708, CD39L709, CD39L710, CD39L711, CD39L712, CD39L713, CD39L714, CD39L715, CD39L716, CD39L717, CD39L718, CD39L719, CD39L720, CD39L721, CD39L722, CD39L723, CD39L724, CD39L725, CD39L726, CD39L727, CD39L728, CD39L729, CD39L730, CD39L731, CD39L732, CD39L733, CD39L734, CD39L735, CD39L736, CD39L737, CD39L738, CD39L739, CD39L740, CD39L741, CD39L742, CD39L743, CD39L744, CD39L745, CD39L746, CD39L747, CD39L748, CD39L749, CD39L750, CD39L751, CD39L752, CD39L753, CD39L754, CD39L755, CD39L756, CD39L757, CD39L758, CD39L759, CD39L760, CD39L761, CD39L762, CD39L763, CD39L764, CD39L765, CD39L766, CD39L767, CD39L768, CD39L769, CD39L770, CD39L771, CD39L772, CD39L773, CD39L774, CD39L775, CD39L776, CD39L777, CD39L778, CD39L779, CD39L780, CD39L781, CD39L782, CD39L783, CD39L784, CD39L785, CD39L786, CD39L787, CD39L788, CD39L789, CD39L790, CD39L791, CD39L792, CD39L793, CD39L794, CD39L795, CD39L796, CD39L797, CD39L798, CD39L799, CD39L800, CD39L801, CD39L802, CD39L803, CD39L804, CD39L805, CD39L806, CD39L807, CD39L808, CD39L809, CD39L810, CD39L811, CD39L812, CD39L813, CD39L814, CD39L815, CD39L816, CD39L817, CD39L818, CD39L819, CD39L820, CD39L821, CD39L822, CD39L823, CD39L824, CD39L825, CD39L826, CD39L827, CD39L828, CD39L829, CD39L830, CD39L831, CD39L832, CD39L833, CD39L834, CD39L835, CD39L836, CD39L837, CD39L838, CD39L839, CD39L840, CD39L841, CD39L842, CD39L843, CD39L844, CD39L845, CD39L846, CD39L847, CD39L848, CD39L849, CD39L850, CD39L851, CD39L852, CD39L853, CD39L854, CD39L855, CD39L856, CD39L857, CD39L858, CD39L859, CD39L860, CD39L861, CD39L862, CD39L863, CD39L864, CD39L865, CD39L866, CD39L867, CD39L868, CD39L869, CD39L870, CD39L871, CD39L872, CD39L873, CD39L874, CD39L875, CD39L876, CD39L877, CD39L878, CD39L879, CD39L880, CD39L881, CD39L882, CD39L883, CD39L884, CD39L885, CD39L886, CD39L887, CD39L888, CD39L889, CD39L890, CD39L891, CD39L892, CD39L893, CD39L894, CD39L895, CD39L896, CD39L897, CD39L898, CD39L899, CD39L900, CD39L901, CD39L902, CD39L903, CD39L904, CD39L905, CD39L906, CD39L907, CD39L908, CD39L909, CD39L910, CD39L911, CD39L912, CD39L913, CD39L914, CD39L915, CD39L916, CD39L917, CD39L918, CD39L919, CD39L920, CD39L921, CD39L922, CD39L923, CD39L924, CD39L925, CD39L926, CD39L927, CD39L928, CD39L929, CD39L930, CD39L931, CD39L932, CD39L933, CD39L934, CD39L935, CD39L936, CD39L937, CD39L938, CD39L939, CD39L940, CD39L941, CD39L942, CD39L943, CD39L944, CD39L945, CD39L946, CD39L947, CD39L948, CD39L949, CD39L950, CD39L951, CD39L952, CD39L953, CD39L954, CD39L955, CD39L956, CD39L957, CD39L958, CD39L959, CD39L960, CD39L961, CD39L962, CD39L963, CD39L964, CD39L965, CD39L966, CD39L967, CD39L968, CD39L969, CD39L970, CD39L971, CD39L972, CD39L973, CD39L974, CD39L975, CD39L976, CD39L977, CD39L978, CD39L979, CD39L980, CD39L981, CD39L982, CD39L983, CD39L984, CD39L985, CD39L986, CD39L987, CD39L988, CD39L989, CD39L990, CD39L991, CD39L992, CD39L993, CD39L994, CD39L995, CD39L996, CD39L997, CD39L998, CD39L999, CD39L1000, CD39L1001, CD39L1002, CD39L1003, CD39L1004, CD39L1005, CD39L1006, CD39L1007, CD39L1008, CD39L1009, CD39L1010, CD39L1011, CD39L1012, CD39L1013, CD39L1014, CD39L1015, CD39L1016, CD39L1017, CD39L1018, CD39L1019, CD39L1020, CD39L1021, CD39L1022, CD39L1023, CD39L1024, CD39L1025, CD39L1026, CD39L1027, CD39L1028, CD39L1029, CD39L1030, CD39L1031, CD39L1032, CD39L1033, CD39L1034, CD39L1035, CD39L1036, CD39L1037, CD39L1038, CD39L1039, CD39L1040, CD39L1041, CD39L1042, CD39L1043, CD39L1044, CD39L1045, CD39L1046, CD39L1047, CD39L1048, CD39L1049, CD39L1050, CD39L1051, CD39L1052, CD39L1053, CD39L1054, CD39L1055, CD39L1056, CD39L1057, CD39L1058, CD39L1059, CD39L1060, CD39L1061, CD39L1062, CD39L1063, CD39L1064, CD39L1065, CD39L1066, CD39L1067, CD39L1068, CD39L1069, CD39L1070, CD39L1071, CD39L1072, CD39L1073, CD39L1074, CD39L1075, CD39L1076, CD39L1077, CD39L1078, CD39L1079, CD39L1080, CD39L1081, CD39L1082, CD39L1083, CD39L1084, CD39L1085, CD39L1086, CD39L1087, CD39L1088, CD39L1089, CD39L1090, CD39L1091, CD39L1092, CD39L1093, CD39L1094, CD39L1095, CD39L1096, CD39L1097, CD39L1098, CD39L1099, CD39L1100, CD39L1101, CD39L1102, CD39L1103, CD39L1104, CD39L1105, CD39L1106, CD39L1107, CD39L1108, CD39L1109, CD39L1110, CD39L1111, CD39L1112, CD39L1113, CD39L1114, CD39L1115, CD39L1116, CD39L1117, CD39L1118, CD39L1119, CD39L1120, CD39L1121, CD39L1122, CD39L1123, CD39L1124, CD39L1125, CD39L1126, CD39L1127, CD39L1128, CD39L1129, CD39L1130, CD39L1131, CD39L1132, CD39L1133, CD39L1134, CD39L1135, CD39L1136, CD39L1137, CD39L1138, CD39L1139, CD39L1140, CD39L1141, CD39L1142, CD39L1143, CD39L1144, CD39L1145, CD39L1146, CD39L1147, CD39L1148, CD39L1149, CD39L1150, CD39L1151, CD39L1152, CD39L1153, CD39L1154, CD39L1155, CD39L1156, CD39L1157, CD39L1158, CD39L1159, CD39L1160, CD39L1161, CD39L1162, CD39L1163, CD39L1164, CD39L1165, CD39L1166, CD39L1167, CD39L1168, CD39L1169, CD39L1170, CD39L1171, CD39L1172, CD39L1173, CD39L1174, CD39L1175, CD39L1176, CD39L1177, CD39L1178, CD39L1179, CD39L1180, CD39L1181, CD39L1182, CD39L1183, CD39L1184, CD39L1185, CD39L1186, CD39L1187, CD39L1188, CD39L1189, CD39L1190, CD39L1191, CD39L1192, CD39L1193, CD39L1194, CD39L1195, CD39L1196, CD39L1197, CD39L1198, CD39L1199, CD39L1200, CD39L1201, CD39L1202, CD39L1203, CD39L1204, CD39L1205, CD39L1206, CD39L1207, CD39L1208, CD39L1209, CD39L1210, CD39L1211, CD39L1212, CD39L1213, CD39L1214, CD39L1215, CD39L1216, CD39L1217, CD39L1218, CD39L1219, CD39L1220, CD39L1221, CD39L1222, CD39L1223, CD39L1224, CD39L1225, CD39L1226, CD39L1227, CD39L1228, CD39L1229, CD39L1230, CD39L1231, CD39L1232, CD39L1233, CD39L1234, CD39L1235, CD39L1236, CD39L1237, CD39L1238, CD39L1239, CD39L1240, CD39L1241, CD39L1242, CD39L1243, CD39L1244, CD39L1245, CD39L1246, CD39L1247, CD39L1248, CD39L1249, CD39L1250, CD39L1251, CD39L1252, CD39L1253, CD39L1254, CD39L1255, CD39L1256, CD39L1257, CD39L1258, CD39L1259, CD39L1260, CD39L1261, CD39L1262, CD39L1263, CD39L1264, CD39L1265, CD39L1266, CD39L1267, CD39L1268, CD39L1269, CD39L1270, CD39L1271, CD39L1272, CD39L1273, CD39L1274, CD39L1275, CD39L1276, CD39L1277, CD39L1278, CD39L1279, CD39L1280, CD39L1281, CD39L1282, CD39L1283, CD39L1284, CD39L1285, CD39L1286, CD39L1287, CD39L1288, CD39L1289, CD39L1290, CD39L1291, CD39L1292, CD39L1293, CD39L1294, CD39L1295, CD39L1296, CD39L1297, CD39L1298, CD39L1299, CD39L1300, CD39L1301, CD39L1302, CD39L1303, CD39L1304, CD39L1305, CD39L1306, CD39L1307, CD39L1308, CD39L1309, CD39L1310, CD39L1311, CD39L1312, CD39L1313, CD39L1314, CD39L1315, CD39L1316, CD39L1317, CD39L1318, CD39L1319, CD39L1320, CD39L1321, CD39L1322, CD39L1323, CD39L1324, CD39L1325, CD39L1326, CD39L1327, CD39L1328, CD39L1329, CD39L1330, CD39L1331, CD39L1332, CD39L1333, CD39L1334, CD39L1335, CD39L1336, CD39L1337, CD39L1338, CD39L1339, CD39L1340, CD39L1341, CD39L1342, CD39L1343, CD39L1344, CD39L1345, CD39L1346, CD39L1347, CD39L1348, CD39L1349, CD39L1350, CD39L1351, CD39L1352, CD39L1353, CD39L1354, CD39L1355, CD39L1356, CD39L1357, CD39L1358, CD39L1359, CD39L1360, CD39L1361, CD39L1362, CD39L1363, CD39L1364, CD39L1365, CD39L1366, CD39L1367, CD39L1368, CD39L1369, CD39L1370, CD39L1371, CD39L1372, CD39L1373, CD39L1374, CD39L1375, CD39L1376, CD39L1377, CD39L1378, CD39L1379, CD39L1380, CD39L1381, CD39L1382, CD39L1383, CD39L1384, CD39L1385, CD39L1386, CD39L1387, CD39L1388, CD39L1389, CD39L1390, CD39L1391, CD39L1392, CD39L1393, CD39L1394, CD39L1395, CD39L1396, CD39L1397, CD39L1398, CD39L1399, CD39L1400, CD39L1401, CD3

Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WATSGTGVFMFLVSCVCSAHSRNCQVWFEGITPLSBNCFINVSASTIYGVIMFDAGSTGT 60
 DB 1 WATSGTGVFMFLVSCVCSAHSRNCQVWFEGITPLSBNCFINVSASTIYGVIMFDAGSTGT 60
 QY 61 RHIVTTFVQMGQQLPILEGVFSVSKGSAFVQPGKAGETVQGLLEVAKGDSIFRSHM 120
 DB 61 RHIVTTFVQMGQQLPILEGVFSVSKGSAFVQPGKAGETVQGLLEVAKGDSIFRSHM 120
 QY 121 KETPVLTAKAGLRLPEHAKALLFEVMEIFRKGSPFLVPGKSNVIMQSDGGLLAWTV 180
 DB 121 KETPVLTAKAGLRLPEHAKALLFEVMEIFRKGSPFLVPGKSNVIMQSDGGLLAWTV 180
 QY 121 KETPVLTAKAGLRLPEHAKALLFEVMEIFRKGSPFLVPGKSNVIMQSDGGLLAWTV 180
 DB 121 KETPVLTAKAGLRLPEHAKALLFEVMEIFRKGSPFLVPGKSNVIMQSDGGLLAWTV 180
 QY 181 NFUTQGLHGRQETVGLDGGASTQITPLQFETKLTGRCYLTSEPMFSTYALYH 240
 DB 181 NFUTQGLHGRQETVGLDGGASTQITPLQFETKLTGRCYLTSEPMFSTYALYH 240
 QY 241 STGLGKAARLALGLAETGDTGHTFSACFLPMLAEWIFGVKYVQGNQGEVGF 300
 DB 241 STGLGKAARLALGLAETGDTGHTFSACFLPMLAEWIFGVKYVQGNQGEVGF 300
 QY 301 EPCYAEVLAVVQGLQHQPVEVQSGFSYASVYDRAVDMDIVDEKGIILKVEFERAK 360
 DB 301 EPCYAEVLAVVQGLQHQPVEVQSGFSYASVYDRAVDMDIVDEKGIILKVEFERAK 360
 QY 361 EVCNMLNETFSGSPFLCNDLSYITALLKQGFADSTVLQTKVNNLETGWALGATPHL 420
 DB 361 EVCNMLNETFSGSPFLCNDLSYITALLKQGFADSTVLQTKVNNLETGWALGATPHL 420
 QY 421 LOSIGISH 428
 DB 421 LOSIGISH 428

RESULT 7
 AD AA144851 standard; Protein; 405 AA.
 AC AA144851;

18-MAY-2000 (first entry)

Human CD39-L66 protein.

CD39-L4; human; CD39-L66; cyprase, nucleotide diphosphatase; NDPase;
 platelet aggregation; antithrombotic; ADP treatment;
 cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
 molecular weight marker; nutritional supplement; tumour; prevention;
 drug targeting; splice variant.

Homo sapiens.

W0200004041-A2.

27-JAN-2000.

16-JUL-1999; 99NO-US16180.

16-JUL-1998; 98US-0118205.

24-JUL-1998; 98US-0122449.

04-FEB-1999; 99US-0244444.

03-MAR-1999; 99US-0273447.

03-JUL-1999; 99US-0350836.

(HYSE)- HYSECO INC.

Ford J. Mulero J;

WPI; 2000-182397/16.

N-P829; AA250356.

PT New nucleic acid encoding human CD39-like protein, useful for treating
 XX and preventing thrombotic disease -

Claim 15; Page 124-125; 125pp; English.

The present amino acid sequence is the CD39-L66 protein, a splice
 variant of the CD39-L4 protein. It is an apyrase and/or nucleotide
 diphosphatase (NDPase), isolated from the human foetal liver-spleen cDNA
 library. The amino acid sequence is: (NH₂)₁ - (NH₂)₂ - (NH₂)₃ - (NH₂)₄ -
 (NH₂)₅ - (NH₂)₆ - (NH₂)₇ - (NH₂)₈ - (NH₂)₉ - (NH₂)₁₀ - (NH₂)₁₁ - (NH₂)₁₂ -
 (NH₂)₁₃ - (NH₂)₁₄ - (NH₂)₁₅ - (NH₂)₁₆ - (NH₂)₁₇ - (NH₂)₁₈ - (NH₂)₁₉ - (NH₂)₂₀ -
 (NH₂)₂₁ - (NH₂)₂₂ - (NH₂)₂₃ - (NH₂)₂₄ - (NH₂)₂₅ - (NH₂)₂₆ - (NH₂)₂₇ - (NH₂)₂₈ -
 (NH₂)₂₉ - (NH₂)₃₀ - (NH₂)₃₁ - (NH₂)₃₂ - (NH₂)₃₃ - (NH₂)₃₄ - (NH₂)₃₅ - (NH₂)₃₆ -
 (NH₂)₃₇ - (NH₂)₃₈ - (NH₂)₃₉ - (NH₂)₄₀ - (NH₂)₄₁ - (NH₂)₄₂ - (NH₂)₄₃ - (NH₂)₄₄ -
 (NH₂)₄₅ - (NH₂)₄₆ - (NH₂)₄₇ - (NH₂)₄₈ - (NH₂)₄₉ - (NH₂)₅₀ - (NH₂)₅₁ - (NH₂)₅₂ -
 (NH₂)₅₃ - (NH₂)₅₄ - (NH₂)₅₅ - (NH₂)₅₆ - (NH₂)₅₇ - (NH₂)₅₈ - (NH₂)₅₉ - (NH₂)₆₀ -
 (NH₂)₆₁ - (NH₂)₆₂ - (NH₂)₆₃ - (NH₂)₆₄ - (NH₂)₆₅ - (NH₂)₆₆ - (NH₂)₆₇ - (NH₂)₆₈ -
 (NH₂)₆₉ - (NH₂)₇₀ - (NH₂)₇₁ - (NH₂)₇₂ - (NH₂)₇₃ - (NH₂)₇₄ - (NH₂)₇₅ - (NH₂)₇₆ -
 (NH₂)₇₇ - (NH₂)₇₈ - (NH₂)₇₉ - (NH₂)₈₀ - (NH₂)₈₁ - (NH₂)₈₂ - (NH₂)₈₃ - (NH₂)₈₄ -
 (NH₂)₈₅ - (NH₂)₈₆ - (NH₂)₈₇ - (NH₂)₈₈ - (NH₂)₈₉ - (NH₂)₉₀ - (NH₂)₉₁ - (NH₂)₉₂ -
 (NH₂)₉₃ - (NH₂)₉₄ - (NH₂)₉₅ - (NH₂)₉₆ - (NH₂)₉₇ - (NH₂)₉₈ - (NH₂)₉₉ - (NH₂)₁₀₀ -
 (NH₂)₁₀₁ - (NH₂)₁₀₂ - (NH₂)₁₀₃ - (NH₂)₁₀₄ - (NH₂)₁₀₅ - (NH₂)₁₀₆ - (NH₂)₁₀₇ -
 (NH₂)₁₀₈ - (NH₂)₁₀₉ - (NH₂)₁₁₀ - (NH₂)₁₁₁ - (NH₂)₁₁₂ - (NH₂)₁₁₃ - (NH₂)₁₁₄ -
 (NH₂)₁₁₅ - (NH₂)₁₁₆ - (NH₂)₁₁₇ - (NH₂)₁₁₈ - (NH₂)₁₁₉ - (NH₂)₁₂₀ - (NH₂)₁₂₁ -
 (NH₂)₁₂₂ - (NH₂)₁₂₃ - (NH₂)₁₂₄ - (NH₂)₁₂₅ - (NH₂)₁₂₆ - (NH₂)₁₂₇ - (NH₂)₁₂₈ -
 (NH₂)₁₂₉ - (NH₂)₁₃₀ - (NH₂)₁₃₁ - (NH₂)₁₃₂ - (NH₂)₁₃₃ - (NH₂)₁₃₄ - (NH₂)₁₃₅ -
 (NH₂)₁₃₆ - (NH₂)₁₃₇ - (NH₂)₁₃₈ - (NH₂)₁₃₉ - (NH₂)₁₄₀ - (NH₂)₁₄₁ - (NH₂)₁₄₂ -
 (NH₂)₁₄₃ - (NH₂)₁₄₄ - (NH₂)₁₄₅ - (NH₂)₁₄₆ - (NH₂)₁₄₇ - (NH₂)₁₄₈ - (NH₂)₁₄₉ -
 (NH₂)₁₅₀ - (NH₂)₁₅₁ - (NH₂)₁₅₂ - (NH₂)₁₅₃ - (NH₂)₁₅₄ - (NH₂)₁₅₅ - (NH₂)₁₅₆ -
 (NH₂)₁₅₇ - (NH₂)₁₅₈ - (NH₂)₁₅₉ - (NH₂)₁₆₀ - (NH₂)₁₆₁ - (NH₂)₁₆₂ - (NH₂)₁₆₃ -
 (NH₂)₁₆₄ - (NH₂)₁₆₅ - (NH₂)₁₆₆ - (NH₂)₁₆₇ - (NH₂)₁₆₈ - (NH₂)₁₆₉ - (NH₂)₁₇₀ -
 (NH₂)₁₇₁ - (NH₂)₁₇₂ - (NH₂)₁₇₃ - (NH₂)₁₇₄ - (NH₂)₁₇₅ - (NH₂)₁₇₆ - (NH₂)₁₇₇ -
 (NH₂)₁₇₈ - (NH₂)₁₇₉ - (NH₂)₁₈₀ - (NH₂)₁₈₁ - (NH₂)₁₈₂ - (NH₂)₁₈₃ - (NH₂)₁₈₄ -
 (NH₂)₁₈₅ - (NH₂)₁₈₆ - (NH₂)₁₈₇ - (NH₂)₁₈₈ - (NH₂)₁₈₉ - (NH₂)₁₉₀ - (NH₂)₁₉₁ -
 (NH₂)₁₉₂ - (NH₂)₁₉₃ - (NH₂)₁₉₄ - (NH₂)₁₉₅ - (NH₂)₁₉₆ - (NH₂)₁₉₇ - (NH₂)₁₉₈ -
 (NH₂)₁₉₉ - (NH₂)₂₀₀ - (NH₂)₂₀₁ - (NH₂)₂₀₂ - (NH₂)₂₀₃ - (NH₂)₂₀₄ - (NH₂)₂₀₅ -
 (NH₂)₂₀₆ - (NH₂)₂₀₇ - (NH₂)₂₀₈ - (NH₂)₂₀₉ - (NH₂)₂₁₀ - (NH₂)₂₁₁ - (NH₂)₂₁₂ -
 (NH₂)₂₁₃ - (NH₂)₂₁₄ - (NH₂)₂₁₅ - (NH₂)₂₁₆ - (NH₂)₂₁₇ - (NH₂)₂₁₈ - (NH₂)₂₁₉ -
 (NH₂)₂₂₀ - (NH₂)₂₂₁ - (NH₂)₂₂₂ - (NH₂)₂₂₃ - (NH₂)₂₂₄ - (NH₂)₂₂₅ - (NH₂)₂₂₆ -
 (NH₂)₂₂₇ - (NH₂)₂₂₈ - (NH₂)₂₂₉ - (NH₂)₂₃₀ - (NH₂)₂₃₁ - (NH₂)₂₃₂ - (NH₂)₂₃₃ -
 (NH₂)₂₃₄ - (NH₂)₂₃₅ - (NH₂)₂₃₆ - (NH₂)₂₃₇ - (NH₂)₂₃₈ - (NH₂)₂₃₉ - (NH₂)₂₄₀ -
 (NH₂)₂₄₁ - (NH₂)₂₄₂ - (NH₂)₂₄₃ - (NH₂)₂₄₄ - (NH₂)₂₄₅ - (NH₂)₂₄₆ - (NH₂)₂₄₇ -
 (NH₂)₂₄₈ - (NH₂)₂₄₉ - (NH₂)₂₅₀ - (NH₂)₂₅₁ - (NH₂)₂₅₂ - (NH₂)₂₅₃ - (NH₂)₂₅₄ -
 (NH₂)₂₅₅ - (NH₂)₂₅₆ - (NH₂)₂₅₇ - (NH₂)₂₅₈ - (NH₂)₂₅₉ - (NH₂)₂₆₀ - (NH₂)₂₆₁ -
 (NH₂)₂₆₂ - (NH₂)₂₆₃ - (NH₂)₂₆₄ - (NH₂)₂₆₅ - (NH₂)₂₆₆ - (NH₂)₂₆₇ - (NH₂)₂₆₈ -
 (NH₂)₂₆₉ - (NH₂)₂₇₀ - (NH₂)₂₇₁ - (NH₂)₂₇₂ - (NH₂)₂₇₃ - (NH₂)₂₇₄ - (NH₂)₂₇₅ -
 (NH₂)₂₇₆ - (NH₂)₂₇₇ - (NH₂)₂₇₈ - (NH₂)₂₇₉ - (NH₂)₂₈₀ - (NH₂)₂₈₁ - (NH₂)₂₈₂ -
 (NH₂)₂₈₃ - (NH₂)₂₈₄ - (NH₂)₂₈₅ - (NH₂)₂₈₆ - (NH₂)₂₈₇ - (NH₂)₂₈₈ - (NH₂)₂₈₉ -
 (NH₂)₂₉₀ - (NH₂)₂₉₁ - (NH₂)₂₉₂ - (NH₂)₂₉₃ - (NH₂)₂₉₄ - (NH₂)₂₉₅ - (NH₂)₂₉₆ -
 (NH₂)₂₉₇ - (NH₂)₂₉₈ - (NH₂)₂₉₉ - (NH₂)₃₀₀ - (NH₂)₃₀₁ - (NH₂)₃₀₂ - (NH₂)₃₀₃ -
 (NH₂)₃₀₄ - (NH₂)₃₀₅ - (NH₂)₃₀₆ - (NH₂)₃₀₇ - (NH₂)₃₀₈ - (NH₂)₃₀₉ - (NH₂)₃₁₀ -
 (NH₂)₃₁₁ - (NH₂)₃₁₂ - (NH₂)₃₁₃ - (NH₂)₃₁₄ - (NH₂)₃₁₅ - (NH₂)₃₁₆ - (NH₂)₃₁₇ -
 (NH₂)₃₁₈ - (NH₂)₃₁₉ - (NH₂)₃₂₀ - (NH₂)₃₂₁ - (NH₂)₃₂₂ - (NH₂)₃₂₃ - (NH₂)₃₂₄ -
 (NH₂)₃₂₅ - (NH₂)₃₂₆ - (NH₂)₃₂₇ - (NH₂)₃₂₈ - (NH₂)₃₂₉ - (NH₂)₃₃₀ - (NH₂)₃₃₁ -
 (NH₂)₃₃₂ - (NH₂)₃₃₃ - (NH₂)₃₃₄ - (NH₂)₃₃₅ - (NH₂)₃₃₆ - (NH₂)₃₃₇ - (NH₂)₃₃₈ -
 (NH₂)₃₃₉ - (NH₂)₃₄₀ - (NH₂)₃₄₁ - (NH₂)₃₄₂ - (NH₂)₃₄₃ - (NH₂)₃₄₄ - (NH₂)₃₄₅ -
 (NH₂)₃₄₆ - (NH₂)₃₄₇ - (NH₂)₃₄₈ - (NH₂)₃₄₉ - (NH₂)₃₅₀ - (NH₂)₃₅₁ - (NH₂)₃₅₂ -
 (NH₂)₃₅₃ - (NH₂)₃₅₄ - (NH₂)₃₅₅ - (NH₂)₃₅₆ - (NH₂)₃₅₇ - (NH₂)₃₅₈ - (NH₂)₃₅₉ -
 (NH₂)₃₆₀ - (NH₂)₃₆₁ - (NH₂)₃₆₂ - (NH₂)₃₆₃ - (NH₂)₃₆₄ - (NH₂)₃₆₅ - (NH₂)₃₆₆ -
 (NH₂)₃₆₇ - (NH₂)₃₆₈ - (NH₂)₃₆₉ - (NH₂)₃₇₀ - (NH₂)₃₇₁ - (NH₂)₃₇₂ - (NH₂)₃₇₃ -
 (NH₂)₃₇₄ - (NH₂)₃₇₅ - (NH₂)₃₇₆ - (NH₂)₃₇₇ - (NH₂)₃₇₈ - (NH₂)₃₇₉ - (NH₂)₃₈₀ -
 (NH₂)₃₈₁ - (NH₂)₃₈₂ - (NH₂)₃₈₃ - (NH₂)₃₈₄ - (NH₂)₃₈₅ - (NH₂)₃₈₆ - (NH₂)₃₈₇ -
 (NH₂)₃₈₈ - (NH₂)₃₈₉ - (NH₂)₃₉₀ - (NH₂)₃₉₁ - (NH₂)₃₉₂ - (NH₂)₃₉₃ - (NH₂)₃₉₄ -
 (NH₂)₃₉₅ - (NH₂)₃₉₆ - (NH₂)₃₉₇ - (NH₂)₃₉₈ - (NH₂)₃₉₉ - (NH₂)₄₀₀ - (NH₂)₄₀₁ -
 (NH₂)₄₀₂ - (NH₂)₄₀₃ - (NH₂)₄₀₄ - (NH₂)₄₀₅ - (NH₂)₄₀₆ - (NH₂)₄₀₇ - (NH₂)₄₀₈ -
 (NH₂)₄₀₉ - (NH₂)₄₁₀ - (NH₂)₄₁₁ - (NH₂)₄₁₂ - (NH₂)₄₁₃ - (NH₂)₄₁₄ - (NH₂)₄₁₅ -
 (NH₂)₄₁₆ - (NH₂)₄₁₇ - (NH₂)₄₁₈ - (NH₂)₄₁₉ - (NH₂)₄₂₀ - (NH₂)₄₂₁ - (NH₂)₄₂₂ -
 (NH₂)₄₂₃ - (NH₂)₄₂₄ - (NH₂)₄₂₅ - (NH₂)₄₂₆ - (NH₂)₄₂₇ - (NH₂)₄₂₈ - (NH₂)₄₂₉ -
 (NH₂)₄₃₀ - (NH₂)₄₃₁ - (NH₂)₄₃₂ - (NH₂)₄₃₃ - (NH₂)₄₃₄ - (NH₂)₄₃₅ - (NH₂)₄₃₆ -
 (NH₂)₄₃₇ - (NH₂)₄₃₈ - (NH₂)₄₃₉ - (NH₂)₄₄₀ - (NH₂)₄₄₁ - (NH₂)₄₄₂ - (NH₂)₄₄₃ -
 (NH₂)₄₄₄ - (NH₂)₄₄₅ - (NH₂)₄₄₆ - (NH₂)₄₄₇ - (NH₂)₄₄₈ - (NH₂)₄₄₉ - (NH₂)₄₅₀ -
 (NH₂)₄₅₁ - (NH₂)₄₅₂ - (NH₂)₄₅₃ - (NH₂)₄₅₄ - (NH₂)₄₅₅ - (NH₂)₄₅₆ - (NH₂)₄₅₇ -
 (NH₂)₄₅₈ - (NH₂)₄₅₉ - (NH₂)₄₆₀ - (NH₂)₄₆₁ - (NH₂)₄₆₂ - (NH₂)₄₆₃ - (NH₂)₄₆₄ -
 (NH₂)₄₆₅ - (NH₂)₄₆₆ - (NH₂)₄₆₇ - (NH₂)₄₆₈ - (NH₂)₄₆₉ - (NH₂)₄₇₀ - (NH₂)₄₇₁ -
 (NH₂)₄₇₂ - (NH₂)₄₇₃ - (NH₂)₄₇₄ - (NH₂)₄₇₅ - (NH₂)₄₇₆ - (NH₂)₄₇₇ - (NH₂)₄₇₈ -
 (NH₂)₄₇₉ - (NH₂)₄₈₀ - (NH₂)₄₈₁ - (NH₂)₄₈₂ - (NH₂)₄₈₃ - (NH₂)₄₈₄ - (NH₂)₄₈₅ -
 (NH₂)₄₈₆ - (NH₂)₄₈₇ - (NH₂)₄₈₈ - (NH₂)₄₈₉ - (NH₂)₄₉₀ - (NH₂)₄₉₁ - (NH₂)₄₉₂ -
 (NH₂)₄₉₃ - (NH₂)₄₉₄ - (NH₂)₄₉₅ - (NH₂)₄₉₆ - (NH₂)₄₉₇ - (NH₂)₄₉₈ - (NH₂)₄₉₉ -
 (NH₂)₅₀₀ - (NH₂)₅₀₁ - (NH₂)₅₀₂ - (NH₂)₅₀₃ - (NH₂)₅₀₄ - (NH₂)₅₀₅ - (NH₂)₅₀₆ -
 (NH₂)₅₀₇ - (NH₂)₅₀₈ - (NH₂)₅₀₉ - (NH₂)₅₁₀ - (NH₂)₅₁₁ - (NH₂)₅₁₂ - (NH₂)₅₁₃ -
 (NH₂)₅₁₄ - (NH₂)₅₁₅ - (NH₂)₅₁₆ - (NH₂)₅₁₇ - (NH₂)₅₁₈ - (NH₂)₅₁₉ - (NH₂)₅₂₀ -
 (NH₂)₅₂₁ - (NH₂)₅₂₂ - (NH₂)

Db 188 FLVGDGVSIMNGTDGVSMTITNFPLSTKTPGGSSVMQDLDGGSTQATFPRVEGT 247
 Qy 217 LEOPTGVLGYLSEFNSTKLYLTHYGLGPKAARLATLGALETE-GTGHTFRSACLPR 275
 Db 248 LQSPGSLTLALRNFRKTYLTVSYLGLGQMSARLATLGALETEGQPAQDKELVPLCLP 307
 Qy 276 WLEAEHFGCVYQVGNZGSENGEFGPCVAELVWVKGLHQPEVORGSPVAFYFYDR 335
 Db 308 SFQSGMEHAEVYVTSQCAASLHEHCAVSEVLRQVHTEVGVDFAFYFYDYL 367
 Qy 336 AVMIDMIDYEGKGLLVYDFEAKSEVCDNLSPGPELQVSLYALVWVGQFND 395
 Db 348 AAGVLIDAEKSGSLWGFDFEAAKYVCTLTQPSQSSFCMLTVSYLLQD-PPGRF 426
 Qy 396 STVLQVTKVKNVETQWALGATPHLQSL 424
 Db 427 SKVLTKRDKINWTSWALGNFHVDSL 459
 RESULT 14
 AB304657
 ID AB304657 standard; Protein: 467 AA.
 XQ Query: March 44:38; Score: 986; E0:23; Length: 467;
 XQ Best Local Similarity: 52.24; Prod No: 4e-87;
 XQ Matches: 203; Conservative: 57; Mismatches: 123; Indels: 6; Gaps: 4;
 DT 11-OCT-2002 (first entry)
 XQ Protein of NOV 15a SEQ ID No 36.
 XQ Cytostatic; antidiabetic; anorectic; metabolic; neurotic; antipsychotic;
 XQ neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
 XQ anti-infective; antidiabetic; antitumor; anti-inflammatory;
 XQ anti-epileptic; antiepileptic; antiepileptic; antiepileptic;
 XQ metabolic disorder; obesity; infectious disease; Alzheimer's disease;
 XQ anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
 XQ immune disorder; hematopoietic disorder; dyalipidemia; chronic disease;
 XQ epilepsy; stroke; mental disorder; schizophrenic disorder; goiter;
 XQ vesicular transport; cystic fibrosis; gastrointestinal disorder;
 XQ diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
 XQ cancer; osteoporosis; rheumatoid arthritis; transgenic animal;
 XQ gene therapy.
 XQ Unidentified.
 XQ H0200246409-A2.
 XQ 13-JUN-2002.
 XQ 06-DEC-2001; 2001NO-US46586.
 XQ 06-DEC-2001; 2000US-251660P.
 XQ 12-DEC-2001; 2000US-255029P.
 XQ 12-DEC-2001; 2000US-255029P.
 XQ 24-JAN-2001; 2001US-263800P.
 XQ 20-FEB-2001; 2001US-265942P.
 XQ 24-APR-2001; 2001US-286183P.
 XQ 24-APR-2001; 2001US-286183P.
 XQ 12-SEP-2001; 2001US-118472P.
 XQ 12-SEP-2001; 2001US-118472P.
 XQ (CURA-) CURAGEN CORP.
 XQ Guo X, Li J, Patrujan M, Shinketa RB, Casman ST, Malyanbar UN;
 XQ Tchernev VT, Vernet CM, Spytek KA, Shenoy SG, Alsebrook JP;
 XQ Edinger S, Peyman K, Stone DJ, Ellerman K, Gangolli SA;
 XQ Boldog FI, Colman SD, Eisen AJ, Padigaru M, Spaderna SK;
 XQ Zarusken BD;
 XQ NPI; 2002-547774/58.
 XQ N-PSDB; A8T05470.
 XQ Novel isolated polypeptide, designated NOVX, useful for treating or

PT preventing cancer, diabetes, obesity, dyalipidemia, anorexia, and
 PT metabolic, neurodegenerative, immune and hematopoietic disorders
 Claim 1, Page 140; 421pp; English.
 The invention relates to an isolated polypeptide, designated NOVX,
 comprising a sequence fully defined in the specification. The isolated
 polypeptide is useful in the manufacture of a medicament for treating the
 syndrome associated with a human disease, preferably a NOVX-associated
 disorder, or for treating or preventing a NOVX-associated disorder in a
 patient, preferably a human patient, its encoding nucleic acid, or a useful
 polypeptide, or for preventing metabolic disorders, diabetes, obesity,
 infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
 disease, Parkinson's disorder, immune disorders, hematopoietic
 disorders, cancer, osteoporosis, rheumatoid arthritis, transgenic
 with obesity, the metabolic syndrome X, wasting disorders associated with
 chronic diseases, and cancer. The isolated protein, its encoding
 polynucleotide or an antibody created from the protein are useful for
 treating or preventing the syndrome associated with a human disease, stroke,
 mental disorders including mood anxiety, schizophrenic disorder, disorders
 of vesicular transport such as cystic fibrosis, diabetes
 mellitus, goiter, gastrointestinal disorders including ulcerative
 colitis, other conditions associated with abnormal vesicle trafficking
 colitis, other conditions associated with abnormal vesicle trafficking
 arthritis. A cell comprising the vector of the invention is useful for
 producing non-human transgenic animals. The polynucleotide of the
 CC invention can be used to treat disorders by gene therapy. This sequence
 represents one of the isolated NOVX proteins of the invention.
 XQ Sequence 467 AA;
 Query: March 44:38; Score: 986; E0:23; Length: 467;
 Best Local Similarity: 52.24; Prod No: 4e-87;
 Matches: 203; Conservative: 57; Mismatches: 123; Indels: 6; Gaps: 4;
 Qy 40 PINVSA--STLVNWDGSGRHHVYTFVOMPOQJLSEGVDSVQGLAVDQ 96
 Db 73 PLGTADGHEVFGIMFDAGSTGTRVHVFTQ-REPRTVTLTHETKALGSLAVAD 131
 Qy 97 PQGASTVQGLLEVARDSIPSHINKTPVVLATAGIALLPKRAKALFEVEFRKSP 156
 Db 132 VEKAGQTRLELVADKQDIPPNKATLHURATKALHFGKQKLVNVEFAS 191
 Qy 157 FLVPGKVSIMNGTDGVSMTITNFPLSTKTPGGSSVMQDLDGGSTQATFPRVEGT 216
 Db 192 FLVGDGVSIMNGTDGVSMTITNFPLSTKTPGGSSVMQDLDGGSTQATFPRVEGT 251
 Qy 217 LEOPTGVLGYLSEFNSTKLYLTHYGLGPKAARLATLGALETE-GTGHTFRSACLPR 275
 Db 252 LQSPGSLTLALRNFRKTYLTVSYLGLGQMSARLATLGALETEGQPAQDKELVPLCLP 311
 Qy 276 WLEAEHFGCVYQVGNZGSENGEFGPCVAELVWVKGLHQPEVORGSPVAFYFYDR 335
 Db 312 SFQSGMEHAEVYVTSQCAASLHEHCAVSEVLRQVHTEVGVDFAFYFYDYL 371
 Qy 336 AVMIDMIDYEGKGLLVYDFEAKSEVCDNLSPGPELQVSLYALVWVGQFND 395
 Db 372 AAGVLIDAEKSGSLWGFDFEAAKYVCTLTQPSQSSFCMLTVSYLLQD-PPGRF 426
 Qy 396 STVLQVTKVKNVETQWALGATPHLQSL 424
 Db 431 SKVLTKRDKINWTSWALGNFHVDSL 459
 RESULT 15
 XQ Query: March 44:38; Score: 986; E0:23; Length: 467;
 XQ Best Local Similarity: 52.24; Prod No: 4e-87;
 XQ Matches: 203; Conservative: 57; Mismatches: 123; Indels: 6; Gaps: 4;
 AC AAM93929 standard; Protein: 456 AA.
 XQ AAM93929
 XQ AAM93929
 XQ AAM93929
 XQ AAM93929
 XQ 06-NOV-2001 (first entry)

QY 396 STVQLTKKNNITCAALGAFHLLQSL 424
 DB 420 SKVLKTRKIDRVETSMALGAFHYIDSL 448
 Search completed: November 13, 2003, 06:18:31
 Job time : 51 secs

XX Human polypeptide, SEQ ID NO: 4100.
 XX Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX Homo sapiens.
 OS EPI130094-A2.
 XX
 XX
 PD 05-SEP-2001.
 XX
 XX 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 XX Oda T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 XX N-PSDB; AAK94892.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 XX Claim 8; SEQ ID NO 4100; 1380bp + sequence listing; English.
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC clones have been determined. The primers for synthesising the full length
 CC cDNA are useful for cloning the cDNA. The primers for synthesising the
 CC cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without the need for a full length human cDNA of the invention. A polypeptide
 CC encoded by a full length human cDNA of the invention is a polypeptide
 CC Note: The sequence data for this patent did not form part of the primed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 XX Sequence 456 AA;
 XX
 Query Match 44.1%; Score 992; DB 22; Length 456;
 Query similarity: 98.5%; Fragment No. 9,5e-17;
 Matches: 202; Conservative: 57; Mismatches: 124; Indels: 6; Gaps: 4;
 QY 40 PINVA--STLYGIMFAGSTGIRHYTVQMGQGLPILGEVDSVPGLSAFVDQ 96
 DB 62 EGTADAGHEVTVYVDELGAGTGVNTHVQPT-RFREFITUTHTPALGSLATD 120
 QY 97 PKGAEIVQGLLEVAQCSIPSHWKTVPVUKATAGLLPHEKAMALFEVKEIFKSP 156
 DB 121 VESKAGSRELDVAHQCPDFWNAFLDLKATVGLKATGELGKQALQKVENVFASP 180
 QY 157 FLVPGKSGVMGSDGLAWVNTVMTFQGLGHQKQETVGLDGGASTQITFLPQKFT 216
 DB 181 FLVDCDSVINGSDGVSQVMIINFTGSLTKTGGSSVCKDLGGSTQVAFLEFVE 240
 QY 217 LEQTPGRLVTFEMFNSTKLYTHSYGLGKLAARLATIAGLETE-GTGHTFRSACLPR 275
 DB 241 LQASPTGFLTALREVFTHKLYSTYGLIGGASRLATLGGVEQCPKNGKELVSPCLSP 300
 QY 276 WLEAMIFGVKVTGCGNCEGEGFPCVAVLVRVAKGHQPEVSGVSFAFSYTYDR 335
 DB 301 SPFGMEHAEVTVFVSGQAASJHELCARVSEVLRQKRVHTEEVHVDVFAFYTYDL 360
 QY 336 AVDTMDIYKGGILVAVDFEKARVCDNLNFTSGSPFLQMDLYITALAGCGCPAD 395
 DB 361 AAGVGLIDAEKGGVLGVDPEIAAKYVCTLTETQPSPPFSQNDLTVVSLLLQE-FGFR 419